Page 10

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produce 2 different mRNAs, one encoding a long form (bcl-XL), the other a short form (bcl-XS), lacking a stretch of 63 amino acids, by differential splicing of the 2nd coding exon to a more proximal 5'-splice donor within the 1st coding exon. Bcl-XS acts as a cominant negative regulator to bcl-XL activity, so it is preferable to use the bcl-XL cDNA for expression. The gene may be modified to facilitate interaction with costimulatory Bax protein and inhibit interaction with antagonistic Bad protein, by modification of the Bcl-2 homology domains BHI and/Or BHZ. The bcl-XL gene may be introduced into T-cells in vivo or ex vivo via gene transfer using introduced into T-cells in vivo or ex vivo wia gene transfer using a vector for HIV infection gene therapy, to augment intracellular bcl-XL protein levels and protect from cell death. A corresponding antisense oligonuclectide or expression vector may be used in gene therapy of e.g. autoimmune disease, graft rejection or graft.

Cherapy of e.g. autoimmune disease, graft rejection or graft.

Cherapy of e.g. autoimmune regulate the immune response in a T-lymphocyte population.

Sequence 926 BP; 220 A; 249 C; 264 G; 193 T;
               8888888888888888888888
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ö aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397 398 ggctggtcgactggatccacagcagtgggggctgggcggagttcacagctctatacgggg 457 424 TIGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 483 277 ggggccgccttgtagccttcttttttggggctgcactgtgtgctgagagtgtcaaca 337 acggggccctggaggaggcgcgcgtctgcgggagggaactgggcatcagtgaggacag 517 724 ACAATGCAGCAGCCGAGAGCCGAAAGGGCCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 783 98 ccgggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157 0; Gaps tegagaccegetteceggegeacettetetgatetggeggeteagetgeatgtgacceag geteageceageacgetteacceaggtetecgaegaacttttteaagggggeeceaact 484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACT 544 GGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGCGCTGTGCGTGGAAAGCGTAGACA Score 131; DB 1; Length 926; Pred. No. 8.7e-24; 0; Mismatches 190; Indels 22.5%; 56.3%; Best_Local Similarity 56.3 Matches 245; Conservative 518 tgctgacggggccg 532 784 GCATGACTGTGGCCG 798 Query Match 218 158 458 278 338

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25-JUN-1999 (first entry)
Base sequence of the plasmid pRx-Bcl-xl-bsr.
Cowpox virus; bsr. viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-xl; FLIP; survivin; IRP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation;
                                                                                                                                                                                                                              08-SEP-1997; JP-259235.
(RPRG-) RPR GENCELL ASIA PACIFIC INC.
                           X33182 standard; DNA; 7372 BP.
                                                                                                                                    inflammatory disease; ss. Synthetic.
                                                                                                                                                                                                                 07-SEP-1998; J04010
                                                                                                                                                                    Homo sapiens.
WO9913073-A2.
                                                                                                                                                                                                  18-MAR-1999.
                                              X33182;
RESULT 15
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WPI; 99-243728/20.

ô 2481 2541 2602 ACCTAGAGCCTIGGATCCAGGAGAACGGCGGCTGGGATACTTTTGTGGAACTCTATGGGA 2661 2362 TIGAACTGCGGTACCGGCGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 2421 517 218 gctcagccagcaacgcttcacccaggtctccgacgaacttttcaagggggccccaact 277 457 98 ccgggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157 Gaps 398 ggctggtcgactggatccacagcagtgggggctggggcggagttcacagctctatacgggg tegagaccegetteceggegeacettetetgatetggeggeteagetgeatgtgacceag 2422 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGGTAAACT 278 ggggccgccttgtagccttctttctctttgggggctgcactgtgtgctgagagtgtcaaca 338 aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 2542 AGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 458 acggggccctggaggaggaggcgcgtctgcgggagggaactggggcatcagtgaggacag ; 0 Query Match 22.5%; Score 131; DB 1; Length 7372; Best Local Similarity 56.3%; Pred. No. 1.3e-23; Matches 245; Conservative 0; Mismatches 190; Indels 158

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2662 ACAATGCAGCAGCCGAGAGCCGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 2721 518 tgctgacgggggccg ö g

Search completed: July 4, 2000, 01:26:24 Job time: 14671 sec

2722 GCATGACTGTGGCCG 2736

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 which tissues they are most highly expressed in (see V59511 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human thymus BCL-XL DNA.

BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease; autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis; multiple sclerosis; ss.

Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            aagctgaggcagaagggttatgtctgtggagctggccccgggggagggcccagcagctgac 120
                                                                                                                                                                                                          71 AAGCIGAGGCAGAAGGGIIAIGICIGIGGAGCIGGCCCCGGGGAGGCCCCAGCAGCIGAC 130
                                                                                                                                                                                                                                       ccgctgcaccaagccatgcgggcagctgagatgagttcgagacccgcttccggcgcacc 180
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                                                                                                 Gaps
                                                                                                                          1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                                                                                       11 ATGGCGACCCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGTGGCAGACTTTGTAGGTTAT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Polyrnucleotide encoding new polyrpeptide(s) that modify apoptosis - and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g. claim 5; Page 94; 127pp; English.

This DNA may be expressed recombinantly for the production of a BCL-X protein, particularly with pcwV plasmids as vectors for expression in mammalian cell cultures. The protein has particular application in cancer cells (failure of programed cell death (PCD))
                                                                                                                                                                                                                                                                                                                                                                                                     131 CCGCTGCAACCAAGCCATGCGGGCAGCKGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
                                                                                                                                                                                                                                                                                            ttetetgatetggeggeteagetgeatgtgaceecaggeteageecageaaegetteaee
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                                                                      DB 1; Length 1864;
                                                                                                                                                                                               455 T;
                                                                                                Indels
                            506 G;
                                                                   Score 423.6; DB 1;
Pred. No. 8.3e-96;
1; Mismatches 5;
                            403 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boise LH, Nunez G, Thompson CB; WPI; 95-052079/07.
                            494 A;
                                                                   72.7%;
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/*tag= a
                                                                                  Best Local Similarity 98.6
Matches 426; Conservative
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DEV CORP.
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05-JAN-1995.
22-JUN-1994; U07089.
22-JUN-1993; US-081448.
(ARCH-) ARCH DEV CORP.
(UNMI ) UNIV MICHIGAN.
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                           1864 BP;
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                           Sequence
                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                   424 TTGAACTGCGGTACCGGCGGCGTTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                    aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   604 AGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGTGGAACTCTATGGGA 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 acggggccctggaggaggcgcgcgtctgcgggaggggaactggggcatcagtgaggacag 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    724 ACAATGCAGCAGCCGAGAGCCGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 783
                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unducing or preventing death of T cells by bcl-XL protein regulation used to increase survival of HIV infected cells or to down:regulate immune responses in immune diseases

Disclosure; Page 51-52; 76pp; English.

This sequence encodes human bcl-XL protein, which protects
T-lymphocytes against cell death. The genomic bcl-X gene may
                                                                                                                                                                                                                                                                                                       geteageceageaegetteacecaggtetecgaegaactttteaagggggeeceaact
                                                                                                                                                                                                                                                                                                                                  484 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGGTAAACT
                                                                                                                                                                                                                                                                                                                                                                 ggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaaca
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or neurodegenerative and autoimmune diseases (premature PCD), e.e.
                                                                                                 Score 131; DB 1; Length 926;
Pred. No. 8.7e-24;
0; Mismatches 190; Indels
                                                   193 T;
                                                   264 G;
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                                                   249 C;
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                                                                                                   22.5%;
56.3%;
                                                 220 A;
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                                                                                                 Query Match
Best Local Similarity 56.3
Matches 245; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995; US-481739.
(ARCH-) ARCH DEV CORP.
(USNA ) US SEC OF NAVY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-1996; U06203
                                                 926 BP;
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                                    sclerosis.
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                                                   Sequence
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                                                                                                                                                                                                                                                                                                   218
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Human secreted protein gene 120 clone HGBG264.

Human secreted protein; fusion protein; gene therapy; protein therapy;

Human; secreted protein; fusion protein; gene therapy; protein therapy;

Human; secreted protein; fusion protein; gene therapy; protein therapy;

diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

developmental abnormality; foetal deficiency; blood; allergy; renal; ds;

immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;

inflammation; ischaemic shock; Alzheimer's disease; restenosis; AlDS;

cognitive disorder; schlozophrenia; prostate; obesity; osteoclast; thymus;

osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                          V59630 standard; DNA; 1864 BP
                                                                                                  19-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-043674.
US-047492.
US-047500.
US-047501.
US-047501.
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US-040162.
US-040333.
US-040334.
US-040334.
US-043311.
US-043312.
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US-043538.
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421 agtgggggctgg 432
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                     421 AGTGGGGGCTGG 432
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23-MAY-1997;
23-MAY-1997;
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23-MAY-1997;
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06-MAR-1998;
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23-MAY-1997;
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07-MAR-1997;
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23-MAY-1997;
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23-MAY-1997;
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                                                                                                                                                                                                                 Homo sapiens
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                                                       RESULT 12
V59630
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New isolated human genes and the secreted polypeptide(s) they encode new isolated human genes and treatment of e.g. cencers, neurological useful for diagnosis and treatment of e.g. cencers, neurological disorders, immune diseases, inflammation or blood disorders at disorders immune diseases, inflammation or blood disorders as Claim i, Page 353-354; 721pp; English.

CC Cloudes a secreted human protein and Appendix as clone ATCC concerted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin cc protein as compared to the human protein only.

CC protein as compared to the human protein only.

CT protein as compared to the human protein only.

CT protein as compared to the human protein only.

Cacid sequences: V99511-V59812; anino acid sequences W74711-W75026) which are useful for preventing, treating or ameliorating medical conditions are useful for preventing, treating or ameliorating medical conditions can be diagnosed by determining the amount of the new polypeptides in a sample cor by determining the presence of mutations in the new polynucleotides.

CC Specific uses are described for each of the 186 polynucleotides, based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R 22-AuG-1997; US-056909.
R 22-AuG-1997; US-056910.
22-AuG-1997; US-056911.
R 05-SEP-1997; US-05769.
R 05-SEP-1997; US-05769.
R 12-SEP-1997; US-05769.
R 12-SEP-1997; US-05769.
A (HUMA-) HUMAN GENOME SCI INC.
I Bednarik DP, Brewer IA, Carter RC, Duan R, Ebner R, Endress GA, I Feng P, Ferrite AM, Fischer CL, Florence RA, Greene JM, Hu JS, Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, I Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z; RWPI, 98-506564/43.
R PP-PSDB; W74948.
                          US-047615.
US-047617.
US-047618.
US-047632.
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US-048964.
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US-056894.
US-056903.
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22-AUG-1997;
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16-JUL-1997;
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22-AUG-1997;
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22-AUG-1997;
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protein associated with Bol-would levels of a Bol-w protein and/or protein associated with Bol-would as a derivative of the mouse Disclosure; Page 38: 52pp; English.

The present sequence is described as a derivative of the mouse bol-w gene (see X2513) and encodes Bol-w protein (see Y0553), a pro-survival member of the Bol-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducting or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bol-w gene can inferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilities as facility, enhancing or otherwise facilities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
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                                                                                                                          An animal model exhibiting reduced levels of a Bcl-w protein and/or
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     16-SEP-1998; AU0764.
16-SEP-1997; AU-009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Adams J, Cory S, Gibson L, Koentgen F, Print C;
P-PSDB; Y05533.
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Claim 2; Fig 12A-12D; 12Opp; English.

This is the nucleotide sequence of the CDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis. Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T;
                                                                                                                                      20-NOV-1998 (first entry)
Nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Bcl-like (HAICH29) protein"
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Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,
Su JY;
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1. .1098
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                                                                     V41925 standard; cDNA; 1098 BP.
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21-JAN-1997; US-034204.
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                                                                                                                             caggictecgacgaactititeaaggggccccaactggggccgccttgtagccttctit 300
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                                                                                                             AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC 120
                                                         1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                     1 ATGCCGACCCCCAGCCTCCAGACACCCCAGACACACCGCTCTAGTGGCTGACTTTGTAGGCTAT 60
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; W36048.
Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                         cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg
                                                                                                                                                                 ttetetgatetggeggeteagetgeatgtgaececeaggeteageceageaecgetteaee
                                                                                                                                                                                                                                      ctctttgggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga
                                                                                                                                                                                                                                                                                                                                                             CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTG
                                                                                                                                                                          CAGGTTTCCGACGAACTTTTCCAAGGGGCCCCTAACTGGGGCCCGTCTTGTGGCCATTCTTT
                                          ö
                         Length 581;
                                           Indels
117
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4.2e-120;
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200
                                           0; Mismatches
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Holmgreen SP;
                          Score 521.8;
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                                 Pred. No.
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 158
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/product= bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-WAR-1997; AU0199.
27-WAR-1996; AU-008965.
(AMRA-) AMRAD OPERATIONS PTY:
Adams JM, Cory S, Gibson LM, I
WPI; 97-489635/45.
                          89.5%;
93.6%;
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 106
                                           Matches 544; Conservative
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                                   Similarity
 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse bcl-w DNA.
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02-OCT-1997.
 Sequence
                           Query Match
                                    Local
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This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w modil brangy, diagnosis, antibody production or screening of potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 atggcgaccccagcctcggccccagacacacgggctctggtggcagacttgtaggttat 60
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Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc
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                                                                                                                                                                                                                                                                                           117 T;
                                                                                                                                                                                                                                                                                                                                                                                                             50; Indels
                                                                                                                                                                                                                                                                                                                                                         Query Match

85.9%; Score 501; DB 1; L

Best Local Similarity 91.4%; Pred. No. 5.5e-115;

Matches 531; Conservative 0; Mismatches 50;
                                                                                                                                                                                                                                                                                           195 G;
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                                                                                                                                                                                                                                                                                           164 C;
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                                                                                                                                                                                                                                                                                              105 A;
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05-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                                           581 BP;
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aagctgaggcagaagggttatgtctgtggagctggcccggggagggcccagcagctgac 120 61 AAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCAGCCGAC 120 cogotgoaccaagccatgogggaagctggagatgagttogagaccogottocggogcaco 180 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCCGGCGCGCC 180

61

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181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCAACGCTTCACC 240

ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc

181

241 caggtctccgacgaacttttcaagggggccccaactggggccgccttgtagccttcttt

GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360 361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420

361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC

301 ctctttgggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga

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For modulating programmed cell death

For modulating programmed cell death

Disclosure: Columns 13-16, 26pp; English.

The present sequence encodes rat bcl-y protein (Rbcl-y). The present sequence encodes rat bcl-y protein (Rbcl-y). The protein also describes human bcl-y protein (Rbcl-y). The protein also describes human bcl-y protein (Rbcl-y and Hbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in comparing the programmed cell death (apptosals and necrosis). Rbcl-y and Hbcl-y and Hbcl-y proteins may be used to treat subjects suffering from: strokes, head trauma, cased in theraptes to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases cell death, aping, spinal cord injuries and amyotrophic lateral cell sclerosis, which may not be apparent. They may also be cell death, aping, spinal cord injuries and amyotrophic lateral corditions where cells under go premature cell death as a customed period. In contrast, if they act as cell death stimulators, can extended period. In contrast, if they act as cell death stimulators, conditions associated with the conditions and auto/hyperimune diseases. They may also be used to cause cell death in, and hence control, parasites.

Sequence 579 BP; 111 A; 157 C; 198 G; 113 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding the rat bol-y protein.

Rat bol-y protein; Rbol-y; human bol-y protein; Hbol-y; bol-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                              540
                       CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel bcl-y homologues of the rat and human bcl-2 protein - useful
                                                                                                                                                                                                  481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG
                                                                  agtgggggctggggggttcacagctctatacggggacggggccctggaggaggcgcgg
                                                                                          cgtctgcgggaggggaactggggcatcagtgaggacagtgctgacggggggcgtggcactg
ggggccctggtaactgtaggggccttttttgctagcaag 579
                                                                                                                                                                                                                                                                                              541 GGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                            X15945 standard; cDNA; 579 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAY-1999 (first entry)
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11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COCE-) COCENSYS INC
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US5883229-A.
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25-NOV-1997;
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481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTG

ggggccctggtaactgtaggggccttttttgctagcaag 579

480

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An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w

Claim 3: Page 34: 52pp: English.

Claim 3: Page 34: 52pp: English.

The present sequence is the mouse bcl-w gene encoding Bcl-w protein seer 105531), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or model carries a mutation is at least one allele of the human or the model carries and sension of the major abnormalities as determined infertile, but possess no other major abnormalities as determined the pastological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherawise facilitating spermatogenesis in animals, or which can induce infertility.
                                                                                                                                          Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                       Gibson L, Koentgen F, Print C;
                                                                                                                                                                                                                                                                                                                             (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                 X25133 standard; DNA; 581 BP.
                                                                                             05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                 16-SEP-1997; AU-009228.
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                                                                                                                                                                                                                                                                                                                                                     Adams J, Cory S, Gi
WPI; 99-243890/20.
                                                                                                                       Mouse bcl-w gene.
                                                                                                                                                                              animal model; ss.
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RESULT
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0; Gaps

35; Indels

0; Mismatches

Best Local Similarity 94.0 Matches 544; Conservative

Query Match

1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60

89.7%; Score 523; DB 1; Length 579; 94.0%; Pred. No. 2.1e-120;

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Presents encodes the rat and human bcl-2 protein - useful for modulating programmed cell death bcl-y homologues of the rat and human bcl-y protein - useful for modulating programmed cell death bcl-y protein (Hbcl-y). The present sequence encodes human bcl-y protein (Rbcl-y). The present sequence encodes human bcl-y protein (Rbcl-y). Rbcl-y and hcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in theraples to treat subjects suffering from: strokes, head trauma, alzehimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral as celerosis-conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used to trias way to develop cell lines which remain viable in culture for used in this way to develop cell lines which remain viable in culture for used in this way to develop cell lines which remain viable in culture for the extended period. In contrast, if they act as cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and cause cell death in, and hence control, pareastes.

Sequence 579 BP; 106 A; 154 C; 208 G; 111 T;
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                                                       25-NOV-1997; 978523.
23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
                                                                                                                                       (COCE-) COCENSYS INC. Guastella J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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P-PSDB; W97392.
                 US5883229-A.
16-MAR-1999.
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Matches 57
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The mammalian bcl.y genes encode a protein that is a member of the bcl.2 family, components in the cell death pathway. The bcl.2 family have both apoptoric activity and the apoptosis blocking activity. bcl.y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.

Sequence 579 BP; 111 A; 157 C; 198 G; 113 T;
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481 CGTCTGCGGGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 540
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Rat bcl-y gene.
ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
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                                                                 /note= "No stop codon given'
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/product= bcl-y
                                                                                                                                                                                                                                                                                                                             V28333 standard; cDNA; 579 BP.
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23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
(COCE-) COCENSIS INC.
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ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
Homo sapiens.
                                                                                                            1 ATGCCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGTGGTTAT
                                                                                                                                                                                         121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
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, enhancing or otherwise facilitating spermatogenesis or which can induce infertility. 581 BP; 104 A; 155 C; 210 G; 112 T;
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                                                 Length 581;
                                                                    5; Indels
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                                                 Score 573; DB 1;
Pred. No. 1e-132;
0; Mismatches 5;
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99.1%;
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                                                Query Match 98.3
Best Local Similarity 99.1
Matches 576; Conservative
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/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V28334 standard; cDNA;
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23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
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WPI; 98-446079/38.
P-PSDB; W61392.
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  inducing,
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CDNA encoding the human bcl-y protein.

Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;

Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;

programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;

head trauma; Alzheimer's Disease; neural; muscular degenerative disease;

multiple sclerosis; myocardial infarction; vitally induced cell death;

aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;

premature cell death; cell death stimulator; prolonged cell life span;

Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                          growth e.g. cancers Claim 3; Column 15/16; 27pp; English.
Claim 3; Column 15/16; 27pp; English.
The mammanlan bcl-y genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y
                                                                                                                                                               falls in the apoptosis activity category. The recombinant protein may administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.
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producing recombinant protein for use in treating uncontrolled cell
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                                                                                                                                                                                                                                                                                                              208 G;
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An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w

Disclosure; Page 36; 52pp; English.

The present sequence is described as a derivative of the human present sequence is described as a derivative of the human pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing certility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or mutine bol-w gene cor in a gene associated with bol-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination.
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                                                                                                                             caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
181 TTCTCTGATCTGGCGCCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human bcl-w gene derivative.
Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                                      agtgggggctgggccttggagttcacagctctatacggggacggggccctggaggaggcgcgg
                                                                                                                                                                                                                                                                                        421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG
                                                                      241 CAGGICICCGACGAACTITITCAAGGGGGCCCCCAACTGGGGCCGCCTTGTAGCCTTCTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
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Adams J, Cory S, Gibson L, Koentgen F, Print
WPI; 99-243890/20.
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16-SEP-1998; AU0764.
16-SEP-1997; AU-009228.
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WO9913710-A1.
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ö 1 atggogaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60 0; Gaps Length 583; 0; Indels 100.0%; Score 583; DB 1; I 100.0%; Pred. No. 3.5e-135; ive 0; Mismatches 0; Best Local Similarity 100. Matches 583; Conservative

Query Match

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Problem 1000 and a sociated with Bcl-w protein and/or protein associated with Bcl-w protein associated with Bcl-w claim 3; Page 31; 52pp; English.

Sclaim 3; Page 31; 52pp; English.

Claim 3; Page 31; 52pp; English.

The present sequence is the human bcl-w gene encoding Bcl-w protein (see Y0530), a pro-survival member of the Bcl-2 family which is undely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male sequences useful for inducing or reducing fertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals inferring the possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of 480 480 481 ogtctgogggagggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540 540 301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360 420 181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240 121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180 181 Incrementation of the content of 241 caggictecgaegaactititeaagggggeeceaactggggeegeetigiageettetit 300 1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60 Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility; 421 agtgggggctgggcggagttcacagctctatacggggacgggggccctggaggaggcgcgg 421 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGCGG 481 CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG 541 ggggccctggtaactgtaggggccttttttgctagcaagtgaa 583 25-MAR-1999.
16-SEP-1998. AU0764.
16-SEP-1997; AU-009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Adams J, Cory S, Gibson L, Koentgen F, Print P-PSDB: Y05530. X25132 standard; DNA; 581 BP 05-JUL-1999 (first entry) Human bcl-w gene. animal model; ss. Homo sapiens. WO9913710-A1. g g 셤 ă g g g 8 δλ 셤 ð g ò ŏ ö ò ð

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

July 3, 2000, 21:21:53 ; Search time 115.05 Seconds (without alignments) 1267.814 Million cell updates/sec Run on:

US-09-155-327B-6 583 1 atggcgaccccagcctcggc......cttttttgctagcaagtgaa 583 Title: Perfect score:

Seguence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

311585 seqs, 125096042 residues Searched:

623170 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

N_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human bcl-w DNA. N	bcl-w gene	bcl-w dene.	bcl-v gen	din	Rat bcl-y gene. Nu	$\boldsymbol{\tau}$	Mouse bcl-w gene.	Mouse bcl-w DNA. N	Mouse bcl-w gene d	Nucleotide sequenc	Human secreted pro	Human thymus BCL-X	Bcl-XL gene. Induc	Base sequence of t	•	Bcl-2 DNA fragment	Human oncogene bcl	gene	Seguence of bcl-2	Base sequence of t	Human BCL2 cDNA. S	Mouse BCL-x gamma	Human bcl-2 gene O		Sequence of bcl-2	Chicken lymphoid B	Human thymus BCL-X	Bax omega protein		Ч	one CB239.		Human adenosine Al
	ID	T96577	X25134	X25132	~	94	æ	X15945	X25133	T96578	X25135	V41925	V59630	081698	T40079	X33182	049815	X33183	054631	086661	N81292	X33184	T33694	V17638	σ.	43	29	081696	9	T48488	097606	V84005	V89057	095494	X53491
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æ	ery	100.0	100.0	98	۲.	97.4	89.7				85.9	72.7	72.7				21.2	•					20.9		20.4	20.4	19.9	19.5	0.6	0.6	6.8	ø.	7.8	7.6	7.5
	COL	583	583	573	567.8	567.8	523	523	521.8	501	501	マ	423.6	131	131	131	123.4	123.4	123.4	123.4	123.4	23	121.8	20.	119	=	15.	m	ς.	52.2	ä	;	45.6	44.4	44
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181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccaggcacgcttcacc 240

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Type III procollag Vector pAC3Al cont	HSV-2 strain SB5 C HSV-2 strain SB5 C	Genomic clone G11F	Human thyroid tran	HSV-2 strain SB5 C	Human LDL receptor	Immunoqlobulin D-r	Bak-2 gene. Screen	Human Cdn-2 DNA. N
Q30849 T16508	V62162 V62176	055750	T05810	V62147	T84509	Q11707	T42139	095493
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35	37	39	40	41	42	43	44	45
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ALIGNMENTS

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cc dominant negative regulator to bcl-XL activity, so it is preferable cc to use the bcl-XL cDNA for expression. The gene may be modified to capital activity may protein and inhibit cinteraction with antagonistic Bad protein, by modification of the contraction with antagonistic Bad protein, by modification of the Bcl-2 homology domains BH1 and/or BH2. The bcl-XL gene may be introduced into T-cells in vivo or ex vivo via gene transfer using a vector for HIV infection gene therapy, to augment intracellular cbcl-XL protein levels and protect from cell death. A corresponding antisense oligonucleotide or expression vector may be used in gene cc therapy of e.g. autoimmune disease, graft rejection or graft. C versus-host disease, to induce cell death (e.g. apoptosis) and cown-regulate the immune response in a T-lymphocyte population. Sequence 926 BP; 220 A; 249 C; 264 G; 193 T;
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DB 1; Length 926;
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23.2%; Score 134.6; DB 1
58.3%; Pred. No. 2.6e-27;
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Best Local Similarity
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RESULT 15
X33182

ID X33182 standard; DNA; 7372 BP.

AC X33182;
DT 25-UUN-1999 (first entry)
DE Base sequence of the plasmid pRx-Bcl-xl-bsr.

Base sequence of the plasmid pRx-Bcl-xl-bsr.

COMPOX v1rus; bsr; viral vector; expression; apoptosis; resistance;

KW crmA; bcl-2; bcl-xl; FLIP; survivin; IAP; ILP; adenovirus; cancer;

KW autoimmune disease; graft rejection reaction; inflammation;

KW inflammatory disease; ss.

Synthetic.

OS Homo sapiens.

PN W09913073-A2.

PD 18-MAR-1999.

PR 07-SEP-1998; J04010.

PR 08-SEP-1998; J04010.

PR (RPRG-) RPR GENCELL ASIA PACIFIC INC.

PI Hamada H;

DR WPI: 99-243728/20.

PR New apoptosis-resistant virus-sensitive cell

PR Scample 2; Page 41-45; 51pp; English.

CC The present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced.

CC The recombinant viruses generated are capable of expressing apoptosis-cc cell line into which an apoptosis resistance gene has been introduced.

CC The recombinant viruses generated are capable of expressing apoptosis-cc associated genes. These can then be used in a variety of diseases for
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which the induction of apoptosis by gene transfer, or where the inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have concountered the problem where if an adenovirus vector capable of expressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated contain a recombinant gene introduced) is established and overcomes the apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the problem. The present sequence represents the human Bcl-xl gene, and sequence 7372 BB; 2353 A; 1749 C; 1649 G; 1621 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2452 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCCTTCG 2511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2632 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 2691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2332 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGCGATTCAGTG 2391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2572 CAGCTIGGAIGGCCACTIACCIGAAIGACCACCIAGAGCCIIGGAICCAGGAGAACGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.2%; Score 134.6; DB 1; Length 7372; 58.3%; Pred. No. 4.5e-27; Live 0; Mismatches 169; Indels 0;
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Best Local Similarity
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Search completed: July 4, 2000, 01:26:28 Job time: 14675 sec

2692 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 2736

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which tissues they are most highly expressed in (see V59511 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human thymus bCL-XL DNA.
BCL-XL, apoptosis; call death; cancer; neurodegenerative disease;
autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis;
multiple sclerosis; ss.
                                                                                                                                                                  250
                                                                                                                                                                                                                                                                                                                                                                                          ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                 0; Gaps
                                                                                                                                          11 ATGCCGACCCCAGCCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apply-nucleotide encoding new poly-peptide(s) that modify apoptosis - and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g. claim 5; Page 94; 127pp; English.

This DNA may be expressed recombinantly for the production of a BCL-X protein, particularly with pcwV plasmids as vectors for expression in mammalian cell cultures. The protein has particular application in cancer cells (failure of programed cell death (PCD))
                                                                                                                                                                                                                                                                       ttetetgacetggcegeteagetacacgtgaceccaggeteageecageaacgetteace
                                                                                                                                                                                                                                                                                                TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC
                                                                                                                                                                                                                                                                                                                            caggiticogacgaactiticcaagggggccctaactgggggccgtcttgtggcaticttt
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                                                                 Length 1864;
                            455 T;
                                                                                          Indels
                          506 G;
                                                                DB 1;
                                                                                       42;
                                                                Score 364.4; DB 1
Pred. No. 7.6e-89;
1; Mismatches 42
                          403 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boise LH, Nunez G, Thompson CB; WPI; 95-052079/07.
                          494 A;
                                                             62.78;
90.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135. .836
/*tag= a
                                                             Query Match 62.73
Best Local Similarity 90.03
Matches 389; Conservative
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05-JAN-1995.
22-JUN-1994; U07089.
22-JUN-1993; US-081448.
(ARCH-) ARCH DEV CORP.
(UNMI.) UNIV MICHIGAN.
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                         1864 BP;
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                         Sequence
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128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
                                                                                                                                                                                                              394 AGCAAGCGCTGAGGGAGGCAGGCGACGATTTGAACTGCGGTACCGGCGGGCATTCAGTG 453
                                                                                                                                                                                                                                                   acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
                                                                                                                                                                                                                                                                                  454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513
                                                                                                                                                                                                                                                                                                                     248 ccgacgaacttttccaaggggccctaactggggccgtcttgtgggcattcttgtctttg 307
                                                                                                                                                                                                                                                                                                                                                        514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 573
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                                                                                                                                               Gaps
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This sequence encodes human bcl.*ZL protein, which protects
T-lymphocytes against cell death. The genomic bcl.*X gene may produce 2 different mRNAs, one encoding a long form (bcl.*XL), the protein a short form (bcl.*XS), lacking a stretch of 63 amino acids, by differential splicing of the 2nd coding exon to a more proximal 5'-splice donor within the 1st coding exon. Bcl.*XS acts as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 368 aggattggatcgtggcctacctggagacacgtctggctgactggatccacagcagtggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; bcl.xL; T-lymphocyte; cell death; gene therapy; HIV; AIDS; antisense; immune disorder; autoimmune disease; graft rejection; graft-versus-host disease; apoptosis; adoptive immunotherapy; ss.
or neurodegenerative and autoimmune diseases (premature PCD), e.e Parkinson's disease, amylotrophic lateral sclerosis and multiple
                                                                                                                                             ö
                                                                                                            Length 926;
                                                       193 T;
                                                                                                       23.2%; Score 134.6; DB 1; Length 58.3%; Pred. No. 2.6e-27; ive 0; Mismatches 169; Indels
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/product= Human bcl-XL protein
                                                     249 C;
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                                                   220 A;
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                                                                                                                         Best_Local Similarity 58.3
Matches 236; Conservative
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07-JUN-1995; US-481739.
(ARCH-) ARCH DEV CORP.
(USNA.) US SEC OF NAVY.
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                                                     926 BP;
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WPI; 96-506159/50
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                                    sclerosis.
                                                     Seguence
                                                                                                          Query Match
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Human secreted protein; gene 120 clone HGBG264.

Human secreted protein; fusion protein; gene therapy; protein therapy;

Human; secreted protein; fusion protein; gene therapy; protein therapy;

diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

developmental abnormality; foctal deficiency; blood; allorgy; renal; developmental abnormality; foctal deficiency; blood; allorgy; renal; diffammation; ischaemic shock; Alzheimer's disease; restenosis; lymphoma;

inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;

cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;

osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; diseation;

endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                            V59630 standard; DNA; 1864 BP
                                                                                                  19-JAN-1999 (first entry)
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US-047596.
US-047597.
US-047599.
US-047600.
US-047601.
US-047612.
US-047613.
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US-043674.

US-047867.

US-047500.

US-047501.

US-047503.

US-047581.

US-047583.

US-047584.

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US-040336.
US-040626.
US-043311.
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421 agtggcggctgg 432
                     421 AGTGGGGGCTGG 432
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02-OCT-1997; US-0610
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07-MAR-1997; U
07-MAR-1997; U
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23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
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23-MAY-1997;
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                                                        RESULT 12
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Per Vision Washington and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological elso disorders, immune diseases, inflammation or blood disorders claim 1; Page 153-154; 721pp; English.

This sequence represents a nucleic acid molecule designated Gene 120 from the human cDNA clone HGBGZ64 (deposited as clone ATCC 97902 and ATCC 209048) which encodes a secreted human protein. The gene can be used to pereste fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. V59502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic are useful for preventing, treating or ameliorating medical conditions are useful for preventing, treating or ameliorating medical conditions are useful for preventing the amount of the new polypeptides in a sample or by determining the amount of the new polypeptides in a sample or becific uses are described for each of the 186 polynucleotides, based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA, Peng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS, Kyaw H, Laffeur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z; P-PSDB; W74848.
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22-AUG-1997; US-056911.
05-SEP-1997; US-057650.
05-SEP-1997; US-057669.
05-SEP-1997; US-057769.
                       US-047615.
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22-AUG-1997; 1
22-AUG-1997; 1
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22-AUG-1997;
22-AUG-1997;
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PPRESENTATION OF THE PRESENTATION OF THE PRESE
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Disclosure: Columns 15-16; 26pp; English.

Disclosure: Columns 15-16; 26pp; English.

The present sequence encodes human bc1-y protein (Hbc1-y). The sequence encodes human bc1-y protein (Rbc1-y). Rbc1-y and Hbc1-y are homologues of the bc1-y protein (Rbc1-y). Rbc1-y and Hbc1-y are homologues of the bc1-y protein (Rbc1-y). Rbc1-y and Hbc1-y are homologues of the bc1-y protein thought to be involved in proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in theraples to treat subjects suffering from: strokes, head trauma, alzewimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis- conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death with the span such as cancer (especially kaposi's sarcoma and prolonged cell life span such as cancer (especially kaposi's sarcoma and angered cancer) death at they may also be used to angered continue diseases. They may also be used to anger cancer chept may also be used to anger cancer) death and auto/hyperinumune diseases. They may also be used to anger cancer cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 T;
                                                                                                                              Novel bcl-y homologues of the rat and human bcl-2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cause cell death in, and hence control, parasites. Sequence 579 BP; 106 A; 154 C; 208 G;
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Best Local Similarity 91.2
Matches 528; Conservative
11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
                                           (COCE-) COCENSYS INC.
                                                                                       WPI; 99-214150/18.
P-PSDB; W97392.
                                                                  Guastella J
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the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products can also be used to detection and diagnosis. Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     þe
                                                                 20-NOV-1998 (first entry)
Nucleotide sequence of the CDNA clone Bcl-like (HAICH29).
Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 12A-12D; 12Opp; English.

This is the nucleotide sequence of the cDNA clone Bcl-like (HAICH29) used in the method of the invention. The products of the clone can lused for treating conditions associated with abnormal expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
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    1098
    /*tag= a
    /product= "Bcl-like (HAICH29) protein"

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                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,
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Best Local Similarity 90.3%; Pred. No. 5.2e-89;
Matches 390; Conservative 0; Mismatches 42
                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                            21-JAN-1997; US-034204.
(AUCK-) AUCKLAND UNISERVICES LTD.
                                 V41925 standard; cDNA; 1098 BP
                                                                                                                                                                                                                                                                          ; US-034205.
                                                                                                                                                                                                                                                          21-JAN-1998; U00960.
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P-PSDB; W59884.
                                                                                                                                        Homo sapiens.
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Homo sapiens.
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Claim 3; Column 15/16; 27pp; English.
The mammalian bcl.y genes encode a protein that is a member of the bcl-2
family, components in the cell death pathway. The bcl-2 family
                                                                                                                     180
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                                                          9
                    Gaps
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producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human bcl-y gene.
ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
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 Length 583;
                    Indels
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                     20;
         Pred. No. 1.3e-125;
 Score 501; DB 1;
                  0; Mismatches
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/product= bcl-y
/note= "No stop c
86.2%;
         91.48;
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V28334;
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                 Matches 531; Conservative
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23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
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Guastella J;
          Similarity
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         Best Local
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Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's bisease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Raposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
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                                                                                                                                                                                                                                                 Score 497.4; DB 1;
Pred. No. 1.2e-124;
0; Mismatches 51;
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11 Similarity 91.2%;
528; Conservative
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16-MAR-1999.
25-NOV-1997; 978523.
23-FEB-1996; US-012201.
                                                                                                                                                                   579 BP;
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auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 48; 86pp; English.
This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene family, extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or
                                                                                                                                                              cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacggggggccgtgggcactg 540
301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
                                 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
                                                                    caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacage 420
                                                                                                         agiggeggetgggeggaetteacagetetatacggggaeggggeeetggaggaegeaegg 480
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27-MAR-1996; AU-008965.
(AMRA-) AMRAD OPERATIONS PTY LTD.
Adams JM, Cory S, Gibson LM, Holmgreen SP;
WPI: 97-489635/45.
P-PSDB; W36647.
Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      can be used to produce recombinant Bcl-w for therapy, diagnosis,
                                                                                                                                                                                                                                    antibody production or screening of potential modulators. Sequence 583 BP; 105 A; 157 C; 210 G; 111 T
                                                                                                                                                                                                                                                                                  BCI-w; apoptosis; bcl-2; cell surviva
diagnosis; degenerative disease; ss.
Homo saplens.
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/*tag= a
/product= bcl-w
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                                      0; Gaps
                                                                        1 atgeegaccecageeteaacececagacacacgegetetagtggetgaetttgtaggetat 60
 DB 1; Length 583;
                                    50; Indels
Score 501; DB 1; I
Pred. No. 1.3e-125;
0; Mismatches 50;
 86.2%;
                   91.48;
                                      Matches 531; Conservative
                     Best Local Similarity
Query Match
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An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w

Brotein associated with Bcl-w

Bisclosure; Page 36; 52pp; English.

Crep present sequence is described as a derivative of the human bisclosure; Page 36; 52pp; English.

Crep present sequence is described as a derivative of the human crep are x25l12) and encodes Bcl-w protein (see Y05512), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility of male animals. Methods are convoluted for the treatment of infertility, or for reducing fertility as modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene con in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination.

They can be used to screen for therapeutic molecules including
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ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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Human bcl-w gene derivative.
Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
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16-SEP-1997; AU-009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Adams J, COLY S, Gibson L, Koentgen F, Print C;
WPI; 99-243890/20.
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for modulating programmed cell death.

Disclosure, Collumns 13-16; 26pp; English.

Disclosure, Collumns 13-16; 26pp; English.

The present sequence encodes rat Del-y protein (HDCl-y). Rbcl-y and Broch encodes rat bel-y protein (HDCl-y). Rbcl-y and Encodes rat bel-y protein thought to be involved in their programmed cell death (apoptosis and necrosis). Rbcl-y and HBCl-y proteins may be used to treat conditions associated with a disruption of proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, seed in therapies to treat subjects suffering from: strokes, head trauma, and the sclerosis, may or act as cell death, as a caperosially multiple sclerosis, myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral cell death, aging spinal cord injuries and amyotrophic lateral sclerosis. Conditions where cells under go premature cell death as a sclerosis or conditions where cells under your perparent. They may also be used in this way to develop cell lines which remain viable in culture for used in this way to develop cell lines which remain viable in culture for used in this way to develop cell lines which remain viable in culture for used in this way to develop cell lines with a cancer (especially kaposi's sarcoma and prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, may also be used to cause cell death in, and hence control, they may also be used to cause cell death in, and hence control, they may also be used to cause cell death in, and hence control, they may also be used to cause cell death in, and hence control, they may also be used to cause cell death in, and hence control, they may also be used to cause cell death in, and hence control protein the may be used to the manner o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.0%; Score 540.6; DB 1; Length 579; Similarity 95.9%; Pred. No. 3.2e-136;
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11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
                                                                                                                                                                                                                                                                      (COCE-) COCENSYS INC.
                                                                                                                                                                          25-NOV-1997; 978523.
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                                                                                    parasite; ss.
                                                                                                                                                      16-MAR-1999.
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Matches 555;
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protein associated with Bol-w

Triangle associated with Bol-w

Claim 3: Page 32: 52pp; English.

Claim 3: Page 32: 52pp; English.

The present sequence is the human bcl-w gene encoding Bcl-w protein

The present sequence is the human bcl-w gene encoding Bcl-w protein

(see Y0530), a pro-survival member of the Bcl-2 family which is

widely expressed and which is essential for spermatogenesis. The

invention relates generally to a method of treatment and to an

inmal model for the identification of molecules and genetic

capuences useful for inducing or reducing fertility of male

sequences useful for inducing or reducing fertility, or

animals. Methods are provided for the treatment of infertility, or

animals. Methods are provided for the sequences is. An animal

model carries a mutation is at least one allele of the human or

mutine bcl-w gene or in a gene associated with bcl-w. Such animals

infertile, but possess no other major abnormalities as determined

infertile, but possess no other major abnormalities as determined

therapeutic molecules including genetic sequences capable of

therapeutic molecules including genetic sequences capable of

inducing, enhancing or otherwise facilitating spermatogenesis in

canimals, or which can induce infertility.

Sequence 581 BP; 104 A; 155 C; 210 G; 112 T;
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                                    481 cgtctgcgggggggggaactgggcatgaqtgagcacagtggtgacggggggccgtggcactg 540
                                                                         481 cercreceseaeseseaecrecesearcasreaseaecastescreacesesesers 540
421 AGTGGGGGCTGGGCCGAGTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGGAGGCACGG 480
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                                                                                                                                                                                                                                                                                                                     Human bcl-w gene.
Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
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                                                                                                                  (HALL-) HALL INST MEDICAL RES WALTER & ELIZA. Adams J. Cory S. Gibson L. Koentgen F. Print C; WPI; 99-243890/20.
                                                                                                                                                                                                                                                        X25132 standard; DNA; 581 BP.
                                                                                                                                                                                                                                                                                                 05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 16-SEP-1998; AU0764.
16-SEP-1997; AU-009228.
                                                                                                                                                                                                                                                                                                                                                            animal model; ss.
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                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                   X25132;
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have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducting, enhancing or otherwise facilitating spermatogenesis in sequence 581 BP; 106 A; 158 C; 200 G; 117 T;
                                                                                                                                                                                                                                                                                                                                                                                                                        caggittccgacgaactttccaagggggccctaactggggccgtcttgtggcattcttt
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ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
                                                                                                                                        DB 1; Length 581;
                                                                                                                                                                  Indels
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                                                                                                                                  96.4%; Score 560.2; DB 1; 97.8%; Pred. No. 1.8e-141; ative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "No stop codon given"
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                                                                                                                                                             568; Conservative
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                                                                                                                                                Local Similarity
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11-FEB-1997, 798897.
23-FEB-1996; US-0122
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                                         Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell producing recombinant protein for use in treating uncontrolled cell growth e.g. cancers
Claim 2: Column 13/14; 27pp; English.

The mammalian bcl.y genes encode a protein that is a member of the bcl-2 family.

The mammalian bcl.y genes encode a protein that is a member of the bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders sequence 579 BP; 111 A; 157 C; 198 G; 113 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding the rat bc1-y protein.

Rat bc1-y protein; Rbc1-y; human bc1-y protein; Hbc1-y; bc1-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                61 aggctgaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgac 120
                                                                                                                                                                                                                                                                                                                                                                                                                                 cogotgoaccaagocatgoggotgotgagacgagtttgagaccogtttccgccgcacc 180
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                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                      93.0%; Score 540.6; DB 1; 95.9%; Pred. No. 3.2e-136; tive 0; Mismatches 24;
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Guastella J;
WPI; 98-446079/38.
P-PSDB; W61391.
                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                       Sest Local
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Disclosure; Page 38; 52pp; mailsh.

Disclosure; Page 38; 52pp; mailsh.

The present sequence is described as a derivative of the mouse color-way gene (see x2513) and encodes Bcl-w protein (see Y05533), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates contentification of molecules and generic sequences useful for inducing or reducing fertility of male animals. Methods are inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene cor in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including
                                                                                                                                                                                          420
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05-JUL-1999 (first entry)
Mouse bcl-w gene derivative.
Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                   caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattcttt
                                                                                                                      caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc
agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg
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                                                                                       CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
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(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Adams J. Cory S, Gibson L, Koentgen F, Print C;
P-PSDB; Y05533.
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Score 581; DB 1; Length 581; Pred. No. 4.7e-147;

100.0%; 100.0%;

Query Match Best Local Similarity

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361 CAAGICCAGGATIGGAICGIGGCCIACCIGGAGACACGICIGGCIGACIGGAICCACAGG 420
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                                                                                                               61 aggetgaggeagaagggttatgtetgtggagetgggeetggggaaggeeeageegeegae 120
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                                                                                                                                                                                                                                                                                                                                          241 caggittocgacgaactittocaagggggccctaactggggccgtcttgtggcattctit 300
0; Gaps
                                     1 atgccgaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctat 60
                                                       The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see Y05531), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse bcl-w gene.
Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc
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16-SEP-1998; AU0764.
16-SEP-1997; AU -009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
GAMBS J, COTY S, Gibson L, Koentgen F, Print (WPI; 99-243890/20.
 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X25133 standard; DNA; 581 BP
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     Matches 581; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             animal model; ss
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

July 4, 2000, 01:26:24; Search time 115.05 Seconds Run on:

(without alignments) 1263.465 Million cell updates/sec

US-09-155-327B-8 581 Title:

1 atgccgaccccagcctcaac.....gccttttttgctagcaagtg 581 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

311585 seqs, 125096042 residues Searched:

623170 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

N_Geneseq_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	bcl-w DNA.	bcl-w	s pcl-w gen	ocl-y gene	encodin	pcl-w	W DNA.	Human bcl-w gene d	bcl-y	cDNA encoding the	Nucleotide sequenc	Human secreted pro	Human thymus BCL-X	Bcl-XL gene. Induc	Base sequence of t		Bcl-2 DNA fragment	Human oncogene bcl	Human bcl-2 gene.	Sequence of bcl-2	Base sequence of t		Chicken lymphoid B	Human bcl-2 gene 0	proto	Sequence of bcl-2	Mouse BCL-x gamma	O.	Human Cdn-3 DNA, N	Human Bax protein	cDNA encoding a hu	mega pr	gene.	Human Cdn-2 DNA. N
QI QI	T96578	X25135	X25133	V28333	X15945	X25132	T96577	X25134	V28334	X15946	V41925	V59630	081698	T40079	X33182	049815	X33183	Q54631	Q86661	N81292	X33184	T33694	081696	073987	X08431	N81293	V17638	081699	Q95494	903260	V84005	T48488	T42139	095493
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P.denitrificans ge BCl-Y cDNA. New is	Human Cdn-1 cDNA.	Bak gene. Screenin Bak CDNA. New Bak-	EST clone CB239, N	Mycobacterium tube	M. tuberculosis im	BSSL/CEL Gene. DNA	Human adenosine Al	M. tuberculosis an
Q13287 T17375	Q95492	142138 V61498	v89057	V44433	V64542	054222	X53491	x01131
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37	36.4	36.4	35.2	34.4	34.4	33.8	33.8	33.6
35 36	37	300	40	41	42	43	44	45
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ALIGNMENTS

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Claim 3; Page 50-51; 86pp; English.

This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheiner's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants furing genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 atgccgaccccagcctcaaccccagacacacgcgctctagtgggctgactttgtaggctat 60
                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases
                                                                                        BCI-w; apoptosis; bc1-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 G;
                                                                                                                                                                                                                                                                                            (AMRA-) AMRAD OPERATIONS PTY LTD. Adams JM. Cory S, Glbson LM, Holmgreen SP; WPI; 97-489635/45. P-PSDB; W36048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 C;
                                                                                                                                               Location/Qualifiers
1..507
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/*tag= a
/product= bcl-w
                              T96578 standard; DNA; 581 BP
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                                                           22-APR-1998 (first entry)
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27-MAR-1997; AU0199.
27-MAR-1996; AU-008965.
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                                                                                Mouse bcl-w DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 94; 127pp; English.

This protein may be expressed recombinantly, particularly with popular plasmids as vectors for expression in mammalian cell cultures. I plasmids as vectors for expression in cancer cells (failure of protein has particular application in cancer cells (failure of programmed cell death (PCD)) or neurodegenerative and autoimmune programmed cell death (PCD)) or neurodegenerative and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-1996;
02-MAY-1996;
04-MAY-1995;
07-JUN-1995;
T-lymphocytes against cell death. A splice variant form, bol-xs, lacks a stretch of 63 amino acids, and is a dominant negative regulator of bcl-XL function. The gene may be modified to facilitate interaction with costimulatory Bax protein and inhibit interaction with antagonistic Bad protein, by modification of the Bcl-2 homology domains BH1 and/or BH2. The bcl-XL gene may be ector for HIV infection gene therapy, to augment intracellular a vector for HIV infection gene therapy, to augment intracellular bcl-XL protein levels and protect from cell death. A corresponding antisense oligonucleotide or expression vector may be used in gene therapy of e.g. autoimmune disease, graft rejection or graftversus-host disease, to induce cell death (e.g. apoptosis) and
                                                                                                                                                                                                                                    Inducing or preventing death of T cells by bcl-XL protein regulation used to increase survival of HIV infected cells or to down:regulate immune responses in immune diseases Disclosure; Page 52-53; 76pp; English.

This is the sequence of a human bcl-XL protein, which protects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diséases (premature PCD), e.g. Parkinson's disease, amylotrophic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bcl-2 homology domain; gene therapy; HIV; AIDS; antisense; immune disorder; autoimmune disease; graft rejection; graft-versus-host disease; apoptosis; adoptive immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcl-XL protein.

Human; bcl-XL; T-lymphocyte; cell death; BH1 domain; BH2 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W05821 standard; Protein; 233 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lateral sclerosis and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 LFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFGGALCVESVDKEMOVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
77; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 AA;
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US-481739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "BH1 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.1%;
53.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "BH2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 616; DB 1;
Pred. No. 7.90e-47;
30; Mismatches 36
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Best Local :
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                                                                                                                                                                                                                     Sequence
                           205
                                                   101 LFGAALCAESVNKEMEPLVGQVQEWMVAXLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160
                                                                                145
                                                                                                                                                       Local Similarity 53.1%;
hes 77; Conservative
161 RLREG-N-WASVRTVLTGAVALGAL 183
                                                                                                          41
                                                                                                                                   85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                             SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
                                                                                                          KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                      233 AA;
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Pred. No. 7.90e-47;
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Search completed: Fri Jun 23 14:13:45 2000 Job time : 14 secs.

121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA 168

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claim 6; Page 50-51; B6pp; English.
This sequence represents a novel protein, bcl-w, encoded by the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators.
Sequence 168 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                       61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                           61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEDLVG 120
                                                                                                                                                                                                                                                                                                                                                                               121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                      1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                            MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
            substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility. Sequence 192 AA;
                                                                                                                                                                                                                                                                1 MATPASAPDTRALVADFVGYKLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                Indels 0;
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                                                                                                                                               Score 1331; DB 1; Length 192; Pred. No. 6.54e-117;
Such animals have disorganised seminferous tubules and are
                                                                                                                                                                                     2; Indels
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Pred. No. 3.67e-104;
8; Mismatches 1;
                                                                                                                                                                                         9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams JM, Cory S, Gibson LM, Holmgreen SP; WPI; 97-489635/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W36048 standard; Protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis; degenerative disease.
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Local Similarity 94.6%;
les 159; Conservative
                                                                                                                                                   95.3%;
93.8%;
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                                                                                                                                                                     Best Local Similarity 93.8%;
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1997; AU0199.
27-MAR-1996; AU-008965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 GALVTVGAFFASK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse bcl-w protein
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Claim 1; Fig 12A-12D; 120pp; English.

This is the amino acid sequence of the CDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory alseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease; autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                        20-NOV-1998 (first entry)
Amino acid sequence of the cDNA clone Bcl-like (HAICH29).
Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                 develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
                                                                                                                                                                         immunological disorder; autoimmune disease; anti-infectious agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotides and encoded polypeptides - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 75.1%; Score 1049; DB 1; Length 365; Best Local Similarity 98.6%; Pred. No. 4.39e-89; Matches 142; Conservative 1; Mismatches 1; Indels
121 QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWA 168
                                                                                                                                                                                                                             23-JUL-1998.
21-JAN-1998; U00960.
21-JAN-1997; US-034205.
21-JAN-1997; US-034204.
31-JAN-1997; US-034204.
(HOCK-) AUCKLAND UNISERVICES LTD.
(HUMA-) HUMAN GENOME SCI INC.
Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 QVQEWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 QVQEWMVAYLETRLVDWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R68887 standard; Protein; 233 AA.
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                                                                    T 13
W59884 standard; Protein; 365 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JAN-1995.
22-JUN-1994; U07089.
22-JUN-1993; US-081448.
(ARCH-) ARCH DEV CORP.
(UNMI ) UNIV MICHIGAN.
Boise LH, Nunez G, Thon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human thymus BCL-XL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 AA;
                                                                                                                                                                                                                                                                                                                                                                              98-414099/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
WO9500642-A.
                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or tumours
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                                                                                                          W59884;
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For modulating programmed cell death

Claim 2: Columns 19-22: 26pp: English.

Claim 2: Columns 19-22: 26pp: English.

The present sequence represents a mammalian bcy-1 protein.

The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y

protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein

thought to be involved in programmed cell death (apoptosis and necrosis).

Rbcl-y and Hbcl-y proteins may be used to treat conditions associated

with a disruption of the cell death pathway. If they act as cell death

inflators, they may be used in therapies to treat subjects suffering

from: strokes, head trauma, Alzheimer's Disease, neural and muscular

degenerative diseases (especially multiple sclerosis), myocardial

infarction, vitally induced cell death, aging, spinal cord injuries and

amyotrophic lateral sclerosis- conditions where cells under go premature

cell death as a result of triggers which may or may not be apparent.

They may also be used in this way to develop cell lines which remain

viable in culture for an extended period. In contrast, if they act as

cell death stimulators, Rbcl-y and Hbcl-y may be used to treat

conditions associated with prolonged cell life span such as cancer

conditions associated with prolonged cell life span such as cancer

conditions associated with prolonged cell life span such as cancer
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Protein sequence of the specification.

Protein sequence of the specification.

Rat bcl.y protein; Rbcl.y; human bcl.y protein; Hbcl.y; bcl.2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; head trauma; Alzheimer's Disease; neural; miscular degenerative disease; and tiple sclerosis; myotrophic lateral sclerosis; cancer; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Raposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRFFF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ATPASAPDTRALVADEVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                        Novel bcl-y homologues of the rat and human bcl-2 protein - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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98.4%; Pred. No. 1.42e-120;
vative 1; Mismatches 2;
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Matches 189; Conservative
25-NOV-1997; US-978523.
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23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
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                      (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (COCE-) COCENSYS INC.
Guastella J;
                                                                      99-214150/18.
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16-MAR-1999.
                                             Guastella J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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for modulating programmed cell death

Disclosure; Columns 19-20; 26pp; English.

The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
protein (Hbcl-y). Rbcl-y and Hbcl-y protein (apoptosis and necrosis).

CC The specification describes rat bcl-y protein (apoptosis and necrosis).

CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
with a disruption of the cell death pathway. If they act as cell death
conditions they may be used in therapies to treat subjects suffering
inhibitors, they may be used in therapies to treat subjects suffering
from: strokes, head trauma, Alzheimer's biseases, neural and muscular
degenerative diseases (especially multiple sclerosis), myocardial
infarction, vitally induced cell death, aging, spinal cord injuries and
amyotrophic lateral sclerosis- conditions where cells under go premature
cell death as a result of triggers which may or may not be apparent.
They may also be used in this way to develop cell lines which remain
viable in culture for an extended period. In contrast, if they act as
cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
conditions associated with prolonged cell life span such as cancer
diseases. They may also be used to cause cell death in, and hence
diseases. They may also be used to cause cell death in, and hence
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Disclosure; Page 39; 52pp; English.

Disclosure; Page 39; 52pp; English.

The present sequence is described of a derivative of mouse Bcl-w
(see also 905531), a pro-survival member of the Bcl-2 family that
is widely expressed and which is essential for spermatogenesis.

The derivative lacks the 24 N-terminal amino acids of Bcl-w.

The invention relates generally to a method of treatment and to an
animal model for the identification of molecules and genetic
sequences useful for inducing or reducing fertility, or for
Rethods are provided for the treatment of infertility, or for
reducing fertility, by modulating spermatogenesis. An animal model
carries a mutation is at least one allele of the human or murine
bcl-w gene (see X25132-35) or in a gene associated with bcl-w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ATPASAPDTRALVADFVGYKLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-UGL-1999 (first entry)
Mouse Bcl-w protein deritvative.
Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1367; DB 1; Pred. No. 1.79e-120;
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Best Local Similarity 97.4%;
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16-SEP-1997; AU-009228.
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181 GALVTVGAFFASK 193
                                               RESULT
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Disclosure; Columns 15-18; 26pp; Engalish.

The present sequence represents rat bcl-y protein (Rbcl-y). Rbcl-y and also describes human bcl-y protein (Bbcl-y). Rbcl-y and Bbcl-y protein may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, cused in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases

CC cell death, aging, spinal cord injuries and amyotrophic lateral

CC cell death, aging, spinal cord injuries and amyotrophic lateral

CC conditions where cells under go premature cell death as a

CC sclerosis- conditions where cells under go premature cell death as a

CC an extended period. In contrast, if they act as cell death stimulators,

CC sclerosis- and auto/hyperimmune diseases. They may also be used to

CC cause cell death in, and hence control, parasites.
                                                                                                                                                                                         The rat bol.y protein.

The rat bol.y protein. Rbol.y; human bol.y protein; Hbol.y; bol.2 homologue; Rat bol.y protein. Rbol.y; human bol.y protein; Bol.y; head death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer; bisase; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Raposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
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121 QVQEMMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel bcl-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death
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                                                                                                                                             W97391 standard; Protein; 193 AA.
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Best Local Similarity 97.48;
watches 188; Conservative
                                                                                                                                                                             20-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    25-NOV-1997; 978523.
23-FEB-1995; US-012201.
11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
(COCE-) COCENSYS INC.
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                                                181 GALVTVGAFFASK 193
                                                                   181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 AA;
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US5883229-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guastella J;
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                                                                                                                                                               W97391;
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Rat bolly protein; Rbolly, human bolly protein; Hbolly, boll-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; head trauma; sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The mammalian boll-y protein is a member of the bol-2 family, components in the cell death pathway. The bol-2 family have both apoptotic activity and the apoptosis blocking activity. bol-y falls in the apoptosis activity. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell growth e.g. cancers
                                                                                                                 Rat bcl-y protein.
bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
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Pred. No. 1.46e-121;
4; Mismatches 1; Indels (
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л 8
W61391 standard; Protein; 193 AA.
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Best Local Similarity 97.4%;
Matches 188; Conservative
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                                                                                   02-OCT-1998 (first entry)
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US-798897.
                                                                                                                                                                                                                                                     11-FEB-1997; 798897.
23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
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                                                                                                                                                                                                                                                                                                                                           (COCE-) COCENSYS INC.
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                                                                                                                                                                                                                                                                                                                                                                                              WPI; 98-446079/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           death is desired
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25-NOV-1997; 9
23-FEB-1996; U
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                                                                                                                                                                       Rattus sp
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                                                           W61391;
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growth e.g. cancers

Example, Column 17/18; 27pp; English.

The mammalian bcl-y protein is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis and the apoptosis blocking activity. bcl-y falls in the apoptosis artivity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                              OVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                          61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                    fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see X25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
                                                                                                                                                                                                                                                                                                                                                 1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                               Gaps
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Nucleic acids encoding B-cell lymphoma-y protein - useful for
producing recombinant protein for use in treating uncontrolled cell
molecules and genetic sequences useful for inducing or reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human bcl-y protein.
bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
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                                                                                                                                                                                                                                                                     98.8%; Score 1380; DB 1; Length 193; 97.9%; Pred. No. 9.23e-122;
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Pred. No. 1.16e-121;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W61392 standard; Protein; 193 AA.
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                                                                                                                                                                                                                                                                                     Local Similarity 97.9%;
nes 189; Conservative
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11-FEB-1997; US-798897.
(COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GALVTVGAFFASK 193
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                                                                                                                                                                                                                                 193 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens.
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                                                                                                                                                                                                               Infertility
                                                                                                                                                                                                                                   Seguence
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The modulating programmed cell death number DCI-z protein - userial per Claim 1; Columns 17-18; 26pp; English.

Claim 1; Columns 17-18; 26pp; English.

The present sequence represents human bcl-y protein (Hbcl-y). The specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in proteins may be used to treat conditions associated with a disruption of proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, closed in therapies to treat subjects suffering from: strokes, head trauma, closed in therapies to disperse, neural and muscular degenerative diseases (especially multiple sclerosis), mayocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral collings where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for the cell death as a cell death as cell death as a cell death as cell de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The human bcl.y protein.

The human bcl.y protein.

Rat bcl.y protein. Rbcl.y; human bcl.y protein; Hbcl.y; bcl.2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's bisease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premarure cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
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                          OVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                             FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel bcl-y homologues of the rat and human bcl-2 protein - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 1.16e-121;
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                                                                                                                                                                                                                                                                                                                                                                                              W97392 standard; Protein; 193 AA.
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Best Local Similarity 98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAY-1999 (first entry)
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11-FEB-1997; US-798897.
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                                                                                                                                                                                                                                                          GALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
US5883229-A.
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Gaps

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2; Indels

Conservative

Local Similarity

190;

Matches

8 ò

Length 193;

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N-PSDB; X25133
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WO9913710-A1.
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            25-MAR-1999
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                                                                                                                                                                                                                                                                                                                                or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases.

or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases.

Claim 6; Page 48; B6pp; English.

This sequence represents a novel human protein, bcl-w, encoded by the cancer or auto-immune diseases, degenerative diseases (e.g. stroke, promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, schaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification.

It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120
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                                      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120
                        QVQEWMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                  Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
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Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 1.91e-123;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                    (AMRA-) AMRAD OPERATIONS PTY LTD.
Adams JM, Cory S, Gibson LM, Holmgreen SP;
WPI; 97-489635/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 3 3 YOSS30 standard; Protein; 193 AA. YOSS30; 05-JUL-1999 (first entry)
                                                                                                                                     T 2
W36O47 standard; Protein; 193 AA.
                                                                                                                                                                                                              diagnosis; degenerative disease
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Best Local Similarity 100.0%;
Matches 193; Conservative
                                                                                                                                                                         22-APR-1998 (first entry)
                                                                                                                                                                                                                                                              27-MAR-1997; AU0199.
27-MAR-1996; AU-008965.
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                                                                                                 GALVTVGAFFASK 193
                                                                                                                                                                                      Human bcl-w protein
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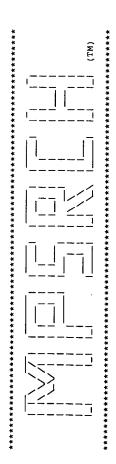
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The natural model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w

25 Claim 27. Page 33.52pp. English.

The present sequence is human Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing for fartility of male animals. Methods are provided for the treatment.

26 fartility of male animals. Methods are provided for the treatment.

27 of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least of a pen associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no cher major abnormalities as determined by histotogical examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise in animals, or which can induce
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Claim 2; Page 35; 52pp; English.
The present sequence is mouse Bcl-w, a pro-survival member of the
Bcl-2 family which is widely expressed and which is essential for
spermatogenesis. The invention relates generally to a method of
treatment and to an animal model for the identification of
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Mouse Bcl-w protein essential for spermatogenesis.
Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
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Pred. No. 4.66e-122;
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Adams J, Cory S, Gibson L, Koentgen F, Print C;
WPI; 99-243890/20.
                                                                                                             Gibson L, Koentgen F, Print
                                                                       HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
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ilarity 99.0%;
Conservative
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16-SEP-1997; AU-009228.
16-SEP-1998; AU0764.
16-SEP-1997; AU-009228.
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Matches 191; Conser
                                                                                                             Àdams J, Cory S, Gi
WPI; 99-243890/20.
N-PSDB; X25132.
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Fri Jun 23 14:13:31 2000; MasPar time 7.29 Seconds 626.869 Million cell updates/sec Run on:

protein - protein database search, using Smith-Waterman algorithm

MPsrch_pp

Tabular output not generated.

>US-09-155-327B-7 (1-193) from US09155327B.pep 1397 Title: Description: Perfect Score: Sequence:

1 MATPASAPDTRALVADFVGY......LTGAVALGALVTVGAFFASK 193

PAM 150 Gap 11 Scoring table:

188963 segs, 23686106 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

1:genesedp a-geneseq36 Database:

Mean 32.637; Variance 140.214; scale 0.233 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SUMMAKIES		
Result No.	Score	Query Match	Query Match Length DB	DB	0.	Description	Pred. No.
-	1397	100.0	193	-	Y05532	Human Bcl-w protein es	1.91e-123
7	1397	100.0	193	٦	W36047	protein.	1.91e-123
m	1383	99.0	193	Н	Y05530	3	4.66e-122
4	1380	98.8	193	Н	Y05531		9.23e-122
S	1379	98.7	193	ч	W61392	Human bcl-y protein.	1.16e-121
9	1379	98.7	193	7	W97392	The human bcl-y protei	1.16e-121
7	1378	98.6	193	ч	W97391	The rat bcl-y protein.	1.46e-121
80	1378	98.6	193		W61391	Rat bcl-y protein.	1.46e-121
σ	1368	97.9	192		W97394	Mammalian bcl-y protei	1.42e-120
10	1367	97.9	192	7	W97393	Protein sequence of th	
11	1331	95.3	192	, 	X05533		6.54e-117
12	1202	86.0	168		W36048	Mouse bcl-w protein.	3.67e-104
13	1049	75.1	365	Н	W59884	Amino acid sequence of	4.39e-89
14	616	44.1	233	-	R68887	Human thymus BCL-XL.	7.90e-47
15	616	44.1	233	-	W05821	Bcl-XL protein.	7.90e-47
16	919	44.1	233	Н	W31530	Human anti-apoptotic B	7.90e-47
17	615	44.0	225	Н	W19396	"Deprenyl" (RTM)-induc	9.87e-47
18	586	41.9	239	-	W87810	A human Bcl-2 protein.	6.14e-44
19	575	41.2	239	-	W87812	A human Bcl-2-alpha pr	7.02e-43
20	575	41.2	239	П	R71404	Human bcl-2 alpha prot	7.02e-43
21	575	41.2	239	Н	R70331	Human bcl-2 protein.	7.02e-43
22	575	41.2	239	Н	R42312	Bcl-2 oncogene product	7.02e-43
23	575	41.2	239	-	W40217	Human bcl-2.	7.02e-43

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FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120

1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

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7.02e-43 7.02e-43 1.36e-42 1.36e-42	1.36e-42 1.36e-42 1.36e-42 6.42e-42 6.42e-42 1.55e-41	3.12e-39 4.84e-39 1.34e-35 1.34e-35 1.34e-35	1.34e-35 1.34e-35 1.49e-32 9.46e-31 9.46e-31 5.77e-20
Sequence of bcl-2-alph Human oncogene bcl-2 p Apoptosis-blocking pro Human Bcl-2 mutant pro A murine Bcl-2 protein	Human BC1-2 wild-type Apoptosis-blocking pro Apoptosis-blocking pro Human BC1-2 mutant pro Human BC1-2	Chicken lymphoid BCL-X Mouse BCL-X gamma. Human thymus BCL-2. Human anti-apoptotic B A human BCl-2-beta pro Human bCl-2 beta pro	Human bcl-2 protein. bcl-2 polypeptide. Sequence of bcl-2-beta Human Bcl-2 mutant pro Apoptosis-blocking pro Human thymus BCL-X1.
P80987 R47344 W01019 W94346 W87811	W94345 W01018 W01020 W94347	R68884 W48312 R68886 W31529 W87813	R70332 W96319 P80988 W94348 W01021 R68885
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41.2 41.2 40.9 40.9	40.04 40.09 40.4 40.2	38 38 38 38 4. 24 4. 25 5. 25	35.7 33.4 32.1 32.1 23.8
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ALIGNMENTS

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			nesis.	Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility; animal model.							ς;		a Dolaw protoin and /or			The present sequence is described of a derivative of human Bcl-w	(see also Y05530), a pro-survival member of the Bcl-2 family that	is widely expressed and which is essential for spermatogenesis	The invention relates generally to a method of treatment and to	animal model for the identification of molecules and genetic	sequences useful for inducing or reducing fertility of male animals.	fertility, or f	reducing fertility, by modulating spermatogenesis. An animal	carries a mutation is at least one allele of the human or murine	bcl-w gene (see X25132-35) or in a gene associated with bcl-w.	noutes and are	substancially intercise, but possess no coner major abnormalities as determined by histological examination. They can be used to	screen for therapeutic molecules including genetic sequences	acilitating	spermatogenesis in animals, or which can induce infertility.		., Length 193;	0; Indels
	A		Human Bcl-w protein essential for spermatogenesis	human, fertili							tgen F, Print		n roub, Azolog. An animal model exhibiting reduced lemels of	70 77 70 70 70 70 70 70 70 70 70 70 70 7	ish.	ed of a deriva	al member of t	s essential fc	to a method c	tion of molecu	r reducing fer	eatment of inf	ng spermatoger	one allele of	a gene assoc	seminierous cu	sacas no ocuer camination	including ge	capable of inducing, enhancing or otherwise facilitating	which can indu		Score 1397; DB 1;	0; Mismatches 0;
	tein; 193 A	entry)	essential fo	-3; Bcl-2; l					28.	DICAL RES WA	son L, Koent		niting reduc	th Bcl-w	52pp; Engl.	is describe	pro-surviva	and which is	s generally	identificat	inducing or	for the tre	oy modulatir	at least o	32-35) or in	Sorganised S	ological es	c molecules	enhancing c	imals, or v			
	standard; Protein; 193 AA	05-JUL-1999 (first entry)	l-w protein	Jenesis; Bcl	iens.	J-A1.	.666	998; AU0764.	997; AU-009228.	(HALL-) HALL INST MEDICAL RES WALTER &	Adams J, Cory S, Gibson L, Koentgen F,	WPI; 99-24389U/20.	model evhil	protein associated with Bcl-w	Disclosure; Page 37; 52pp; English.	ent sequence	o Y05530), a	expressed ?	ntion relates	odel for the	s useful for	ire provided	fertility, 1	mutation is	le (see X251	ally infort	nined by hist	or therapeuti	of inducing,	penesis in ar	193 AA;	10	193; Conservative
RESULT 1	Y05532 st Y05532;	05-JUL-19	Human Bc	Spermatogenes	Homo sapiens	WO9913710-A1.	25-MAR-1999.	16-SEP-1998;	16-SEP-1997;	(HALL-)	Adams J,	WPI; 99-243890/ N-BCDB: 935134	An animal	protein	Disclosur	The prese	(see also	is widely	The inver	animal mo	sednences	Methods a	reducing	carries a	DCI-W ger	such anti	as determ	screen fo	capable c	spermatog	Sequence		Matches 19
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Best Local Similarity 56.8%; Pred. No. 7.9e-21;
Matches 249; Conservative 0; Mismatches 189; Indels
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Sus scrofa
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BETPERERFEYERSINGMRSWHLADSPAVNGATGHSSSLDAREVLDMAAVKQALREAGDE
FELRYRRAFSDLTSQLTSTHTFGTVYQSFEQVVNELFROVNWGRIVASSSFGGALCVES
VEKEMQVLVSRIASMMATYLNDHLEPWIQENGWDTFVDLYGNNTAPESRKGQERFUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 726)
Tilly,J.L., Tilly,K.I., Kenton,M.L. and Johnson,A.L.
Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels Endocrinology 136 (1), 232-241 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 162917] from the original journal article. Location/Qualifiers
agatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgcggc 400
                                                                                                                                 461 gggccctggaggaggaggcgtctgcgggagggaactgggcatcagtgaggacagtgc 520
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                         S76513 726 bp mRNA ROD 26-SEP-199:
bcl-x=apoptosis inhibitor [protooncogene] [rats, ovary, mRNA
Partial, 726 nt].
                                                                                   101 tggtcgactggatccacagcagtggggggttgggcggagttcacagctctatacggggacg
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Pred. No. 2.1e-21;
]; Mismatches 188;
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/note="apoptosis inhibitor"
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/db_xref="G1:998482"
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/organism="Rattus
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AETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPWAAVKQALREAGDEFELRYR
RAFSDLTSQLHITPCTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQ
VLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLTGM
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Direct Submission
Submitted (13-DEC-1999) Biochemistry, SUNY at Buffalo, 3435 Main
Street, Buffalo, NY 14214-3000, USA
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                  372 CAGTATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTCGGGATGGGGTAAACTGGG 431
                                                                                                                                                                                                    341 agatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgcggc 400
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312 AACTGCGGTACCGGAGAGCATTCAGTGATCTAACATCCCAGCTTCATATAACCCCCAGGGA 371
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Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 720)
Lee.T.L. and Canty,J.M.
PCR Cloning of a Porcine bcl-xL cDNA from Heart
                                                        221 cagcccagcaacgcttcacccaggtctccgacgaactttttcaagggggccccaactggg
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/protein_id="AAF33212.1"
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/db_xref="taxon:9823"
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Lee, T.L. and Canty, J.M.
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REPEALNGWRSWHLADSPAYWGATGHSSLDAREVIPMAANYGALREAGDEFELRYR
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VLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESRKGQEFFNRWFLTGM
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RETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPWAAVKQALREAGDEFELRYR
RAFSDLTSQLHITPGTAYQSFEQDTFVDLYGNNAAABESRKGQERFNRWFLTGMTVAGV
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                                                                                              /tissue_type="brain"
/clone_lib="hippocampal cDNA libr. and genomic DNA libr."
/clone="X9, X31"
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                                                                                                                                                                                                                                                                                                                                                                                                   'note="smaller form due to splicing"
                                            /organism="Rattus norvegicus"
/db_xref="taxon:10116"
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/db_xref="GI:607178"
                                                                                                                                                                                                                                         'protein_id="CAA57886.1"
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/gene="bcl-x"
                                                                             /dev_stage="embryonic"
                Location/Qualifiers
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Tilly, J.L., Tilly, K.I., Kenton, M.L. and Johnson, A.L. Direct Submission

Direct Submission

Bubmitted (28-AUG-1995) Jonathan L. Tilly, Department of Obstetrics and Gynecology/Vincent Center for Reproductive Biology,

Massachusetts General Hospital/Harvard Medical School, 32 Fruit Street, Boston, MA 02114, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation-*MSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPE
RETPSAINGNRSWHLADSPAVNGATCHSSSLDAREVLPMAAKQALREAGDEFELRYR
RETPSAINGNRSWHLADSPAVNGATCHSSSLDAREVLPMAKKQALREAGDEFELRYR
RAFSDLTSQLHITPGTYOFFGOVVNETFRDGVNMGRIVASSSFGGALCVESVDKEMO
VLVSRLASWMATYLNDHLEPWIQENGGWDTFVDLYGNWTAPESRKGQBERNRWFLTGM
                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 726)
Tally, A.L., Tilly, K.I., Kenton, M.L. and Johnson, A.L.
Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels Endocrinology 136 (1), 232-241 (1995)
                                                                                                                                    RND 4963 726 bp mRNA ROD 02-OCT-1995 Rattus norvegicus programmed cell death repressor BCL-X-Long mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="programmed cell death repressor; Bcl-2 homolog; long isoform of BCL-X; member of the bcl-2 gene family" /codon_start=1
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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/protein_id="AAA77686.1"
/db_xref="GI:1004377"
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/db_xref="taxon:10116"
/tissue_type="ovary"
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/codon_start=1
/product="Bc1-x"
/protein_id="AaA19257.1"
/db_xref="G1:505699"
/translation="MSQSNRELVVDSLSYKLSQKGYSWSQFSDVEENRTEAPEETEPE
                                                                                  RETESAINGNPSWHLADSPEVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYR
RAFSDLTSQLHITPGTAYQSPEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQ
VLVSRIASWNATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGM
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Shiraiwa, N., Inohara, N., Okada, S., Yuzaki, M., Shoji, S. and Ohta, S. An additional form of rat Bcl-x, Bcl-xbeta, generated by an unspliced RNA, promotes apoptosis in promyeloid cells
J. Biol. Chem. 271 (22), 13258-13265 (1996)
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Direct Submission
Bubmitted (24-SEP-1996) Division of Biochemistry, Institute of Gerontology, 1-396 Kosugi-cho, Nakahara-ku, Kawasaki City 211, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgcggc 400
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                                                                                                                                                                                                                                                                                                                                                                                                        331 AACTGCGGTACCGGAGAGCATTCAGTGATCTAACATCCCAGCTTCATATAACCCCAGGGA 390
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                              Length 764;
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Pred. No. 1.8e-22;
0; Mismatches 185; Indels
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Rattus norvegicus Bcl-xalpha mRNA, complete cds.
U72350
                                                                                                                                                          229 g
                                                                                                                                         TVAGVVLLGSLFSRK
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57.9%;
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Matches 254; Conservative
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/traislation="MSOSNRELVVDFLSYKLSOKGYSWSOFSDVEENRTEAPEFTEPE
RETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPWAAVKQALREAGDBFELRYR
REASDLTGOLHITPGTAXQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMO
VLVSRILASWMATYLUNHLEPWIQENGGWDTFVDLYGNNAAAESRKGOERFNRWFLTGM
TVAGVVLLGSLFSRK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 agacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccaggct 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 tggtcgactggatccacagcagtgggggctgggcggagttcacagctctatacggggacg 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 AACTGCGGTACCGGAGGCATTCAGTGATCTAACATCCCAGCTTCATATAACCCCAGGGA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 agatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgcggc 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 GGGAGGTAATCCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGTTTG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-DEC-1994
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Rattus.
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( pases I to 2232)

Michaelidis,T.M.

Direct Submission
Submitted (04-NOV-1994) T.M. Michaelidis, Max-Planck-Inst.

Psychiatry, Dept of Neurochemistry, 82152 Martinsried, FRG
Michaelidis,T.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 cagcocagcaacgcttcacccaggtctccgacgaactttttcaagggggcccaactggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 CAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTCGGGATGGGGTAAACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     604 TAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGACACTTTTGTGGATCTCTACGGGAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.5%; Score 143; DB 12; Best Local Similarity 57.9%; Pred. No. 1.6e-22;
                       /organism="Rattus norvegicus"
/db_xref="taxon:10116"
72. .773
                                                                                                                                                                                                                                                                                                                                            381
                                                                                                                                     /product="Bc1-xalpha"
/protein_id="AAB17353.1"
/db_xref="G1:1622937"
                                                                                                                                                                                                                                                                                                                                      477 g
Location/Qualifiers
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                                                                                                                      /codon_start=1
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Matches 370;
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AUTHORS
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DLGSRALVEDLVRYKLCQRSLVPEPSGAASCALHSAMRAAGDEFEERFRQAFSEISTQ
IHVTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (02-NOV-1994) J.A. Cruz-Reyes, National Institute of
Medical Research, NIMR/MRC Mill Hill, The Ridgeway Road, London NW7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVTYLETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGAL.
MTVGALFASK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning, characterization and expression of two Xenopus bcl-2-like cell-survival genes
Gene 158 (2), 171-179 (1995)
                          301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
                                                                  caggiciccgacgaactititicaagggggccccaactggggccgccttgtagccticttt 300
                                                                                                                                                                             361 caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc 420
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia;
Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                            01-JUL-1997
            181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 749
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/dev_stage="28-30 (tailbud tadpole)"
/clone_lib="lambda ZapII:R1"
                                                                                                                                                                                                                                                                                                                            VRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SWISS-PROT:091827"
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/db_xref="GI:1334682"
                                                                                                                                                                                                                                                                                                                            mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="pKS+:xR1"
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                                                                                                                                                                                                                                                                                                                         XLR1 749 bp
X.laevis R1 mRNA.
X82462
X82462.1 GI:575421
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3. .689
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African clawed frog.
Xenopus laevis
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Cruz-Reyes, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 749)
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ORGANISM
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                                                                  241
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VERSION
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TITLE
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Score 238.2; DB 4; Length 749; Pred. No. 9.3e-44;

40.9%;

Query Match Best Local Similarity

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Submitted (13-JUN-1994) J. Marie Hardwick, Neurology, Johns Hopkins
School of Medicine, 600 North Wolfe St., Baltimore, MD 21287-7681,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wesselingh, S.L., David, G.L., Choi, S., Veliuona, M. and Hardwick, J.M. Cloning and expression of rat bcl-x in cultured neurons Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                   192 AGTCTGGTTCCGGAGCCT-----TCAGGAGCAGCAGCATCCTGTGCTTTGCATTCGGCT 242
                                                                                                                                                                                                                                          136 atgogggcagctggagatgagttcgagacccgcttccggcgcaccttctctgatctggcg 195
                                                                                                                                                                                                                                                                      gotcagotgcatgtgaccccaggctcagcccagcaacgcttcacccaggtctccgacgaa 255
                                                                                                                                                                                                                                                                                                                                                                  ctgtgtgtgctgagagtgtcaacaaggagatggaaccactggtgggacaagtgcaggagtgg 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 atggtggcctacctggagacgcggctggtcgactggatccacagcagtgggggctgggcg 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 ATGGTGACATATCTGGAGACAAACCTGAGAGACTGGATTCAGAGCAATGGTGGCTGGAAT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 gagttcacagctctatacggggacggggccctggaggaggcgcggcgtctgcgggagggg 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       496 aactgggcatcagtgaggacagtgctgacgggggccgtggcactgggggccctggtaact 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 TCTGACCTAGGATCCCGGGCTTTGGTAGAGGATTTGGTGAGGTACAAGTTATGCCAGCGT 191
                                                                                                                                              76 ggttatgtctgtggagctggccccggggagggcccagcagctgacccgctgcaccaagcc 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tcggccccagacacacgggctctggtggcagactttgtaggttataagctgaggcagaag 75
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Rattus norvegicus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eukaryota, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543 GGGTTTCTAACTCTATATGGGGATGGTGCCATAGAAGAAGCCAGGAGGCAACGTGAGGGG
6
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Rattus norvegicus Bcl-x (bcl-x) gene, complete cds.
U10579
Indels
Mismatches 188;
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1. .764
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
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39. .740
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39. .740
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Conservative
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/note="matching EMBL:AA452257; Identified using the e-PCR software (G. Schuler)"
/note="matching EMBL:AA167748; Identified using the e-PCR software (G. Schuler)" 82162. .82297 /standard_name="H79035"
                                                                      /note="matching EMBL:H79035; Identified using the e-PCR software (G. Schuler)"
93575. 93803
/standard_name="AA007328"
/standard_name="AA007328; Identified using the e-PCR software (G. Schuler)"
107753. .107946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name="R87257"
/note="matching EMBL:R87257; Identified using the e-PCR software (G. Schuler)"
138457. 138733
/standard_name="R59134"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name="M78946"
/note="matching EMBL:M78946; Identified using the e-PCR
software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="matching EMBL:N91549; Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89821 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 89880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="matching EMBL:R94929; Identified using the e-PCR software (G. Schuler)"
107991. .108176
//standard_name="D11677"
/note="matching EMBL:D11677; Identified using the e-PCR software (G. Schuler)"
128383. .128521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="matching EMBL: W78986; Identified using the e-PCR software (G. Schuler)"
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Pred. No. 2.1e-85;
0; Mismatches 6; Indels 0; G
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                                                                                                                                                                                                                                                                                                                                            /standard_name="H22648"
/standard_name="H22648"
software (G. Schuler)"
128415. .128539
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50873 a 45668 c 47123 g 52623
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161612. .161756
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Best Local Similarity 98.6%;
Matches 427; Conservative (
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Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-124D2 of
RPCI-11 library from chromosome 14 of Homo sapiens (Human),
ALO49829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-OCT-1999) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr con oct 28, 1999 this sequence version replaced gi:4972127.

IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence 1s in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name="AA908790"
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software (G. Schuler)"
80431. .80564
                                                                                                                                                                                                                                              cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcatg 540
                                                                                                                                                                      caagigcaggagiggatggiggcctacciggagacgcggctggicgactggatccacagc 420
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                 ttetetgatetggeggeteagetgeatgtgaeeecaggeteageeeageaaegetteaee
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78257. .78396
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RLREGNWASVPRTGANLGALUTYCAFFASK"

1158 c 200 g 117 t
Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
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                                           Submitted (03-JUN-1996) Molecular Biology Unit, The Walter ar
Eliza Hall Institute of Medical Research, Po Royal Melbourne
Hospital, Parkville, Victoria 3050, Australia
Location/Qualifiers
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                                                                                                                                                                                                                               /gene="bcl-w"
/note="promotes cell survival; Bcl-2 homolog"
/codon_start=1
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Best Local Similarity 93.6%; Pred. No. 2.4e-107
Matches 545; Conservative 0; Mismatches 37
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1. .582
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1. .582
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/translation="MatPaSTPDTRALVADFVGXKLROKGYVCGAGPGEGPAADPLHQ
AMAGAGEFETRRERETBADLHYPGSAQQNETGVSDELFCGGPNWGRLVAFFVF
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RLREGNWASYPRYVLTGANALGALVTVGAFFASK"
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                                                                                                                                                            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3476)
Ross.A.J., Waymire, K.G., Moss, J.E., Parlow, A.F., Russell, L.D. and
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                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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                                                                                                                                                                                                                                                     Chases 1 to 3476)
Ross, A.J. and MacGregor, G.R.
Direct Submission
Submitted (21-OCT-1997) Center for Molecular Medicine,
University, 1462 Clifton Road, Atlanta, GA 30322, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                 Mus musculus BCL-W (Bcl-w) mRNA, complete cds. AF030769
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0; Mismatches 37;
                                                                                                                                                                                                                           Bcl-w is required for testis homeostasis Unpublished
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                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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Matches 545; Conservative
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/brotein_id="RAC64200.1"
/brotein_id="RAC64200.1"
/translation="WARTPASTPDTRALVADEVGYKLRQKGYVCGAGFGEGPRADPLHQ
AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQORFTQVSDELFQGGPNWGRLVAFFVF
RLACALCAESTVREMEPLVGQVQDWMYTYLETRLADWIHSSGGWAEFTALYGDGALEEAR
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                                                                                                                                                                                Score 527.6; DB 12; Length 582;
Pred. No. 2e-108;
0; Mismatches 34; Indels 0;
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                                         /note="Bcl-2 family member"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1 from patent US 5789201.
                                                                /product="Bcl-w"
                                                     /codon_start=1
1. .582
/gene="bcl-w"
1. .582
                             /gene="bcl-w"
                                                                                                                                                                                 90.5%;
94.2%;
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Best Local Similarity 94.2<sup>3</sup>
Matches 548; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 582)
Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. Docl-w, a novel member of the bcl-2 family, promotes cell survival 60558615
                                                                                                                                                                                                                                                                             420
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Mus musculus Bcl-w (bcl-w) mRNA, complete cds.
U59746
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Pred. No. 2.1e-107;
0; Mismatches 35;
Guastella,J.
Genes coding for bcl-y a bcl-2 homologue
Patent: US 5789201-A 1 04-AUG-1998;
Location/Qualifiers
                                                                                /organism="unknown"
157 c 198 g
                                                                                                                                                        Query Match 89.7%;
Best Local Similarity 94.0%;
Matches 544; Conservative
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AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQORFTQVSDELFQGGPNWGRLVAFFVF
RAALCAESVNREMEPLVGQVQBWNVAYLETRLADWIHSSGGRAEFTALYGDGALBERAR
RLREGNWSVRYUTIGAAAGALVYVGAFFASK"
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                                                                        Length 3542;
                                                                      tch 98.6%; Score 575; DB 9; Length 35 al Similarity 99.1%; Pred. No. 4.2e-119; 578; Conservative 0; Mismatches 5; Indels
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Patent: US 5789201-A 2 04-AUG-1998;
Location/Qualifiers
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Hammer's.'s, SkejLosa/Y. and Lindholm,D.
Differential expression of Bcl-w and Bcl-x mRNA in the developing
and adult nervous system
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Rattus.
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Direct Submission
Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
University, Box 587, BMC, Uppsala 751 23, Sweden
Location/Qualifiers
                                                                                                                                                                                                                                                               61 aagctgaggcagaagggttatgtctgtggagctggccccgggggagggcccagcagctgac
                                                                                                                                                                        caagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatccacagc
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds
  Length
                         Indels
Score 567.8; DB 5;
Pred. No. 2.1e-117;
0; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="brain"
/dev_stage="postnatal"
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97.4%;
98.8%;
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Query Match 97.4
Best Local Similarity 98.8
Matches 572; Conservative
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AMARAGDEFETRERRFFSDLAAQLHYPGSAQQRFTQYSDELRQGGPWGRLVAFFVF
GAALCAESVNKEMEPLYGQYOEWMVAYLETRLADWIHSSGGWAEFTALXGDGALEEBAR
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Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Euthoria; Primetes; Catarrhini; Hominidae; Homo.

1 (bases 1 to 582)

Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. Obocogene 13 (4), 665-675 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 aagctgaggcagaagggttatgtctgtggagctggccccgggggagggcccagcagctgac 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 240
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99.0%; Score 577.2; DB 10; Length 582;
Best Local Similarity 99.5%; Pred. No. 1.6e-119;
Matches 579; Conservative 0; Mismatches 3; Indels 0:
                            HSU59747 582 bp mRNA
Human Bcl-w (bcl-w) mRNA, complete cds.
U59747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="promotes cell survival"
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/chromosome="14"
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/product="Bcl-w"
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3 (sites)
Magase, T., Seki, N., Ishikawa, K., Ohira, M., Kawarabayasi, Y.,
Ohara, O., Tanaka, A., Kotani, H., Miyajima, N. and Nomura, N.
Prediction of the coding sequences of unidentified human genes. VI.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of coNA clones from cell line KG-1 and brain
DNA Res. 3 (5), 321-329 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (sites) Nagase,T., Seki,N., Ishikawa,K. and Nomura,N. Nagase,T., Seki,N., Ishikawa,K. and Nomura,N. Prediction of the coding sequences of unidentified human genes.VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from human cell line KG-1 and brain Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-AUG-1996) to the DDBJ/EMBL/GenBank databases. Nobunoura, Kazusa DNA Research Institute, Gene Structure 1: 1532-3 Yana, Kisarazu, Chiba 292, Japan (E-mail:cdnainfo@kazusa.or.jp, URL.http://www.kazusa.or.jp, Tel:0438-52-3930, Fax:0438-52-3931)
                                                                     480
421 agtgggggctgggcggagttcacagctctatacggggacgggggccctggaggaggcgcgg 480
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Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 3542)
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Human mRNA for KIAA0271 gene, complete cds.
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/sex="male"
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177. .758
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-638.388 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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U10579 Rattus norv
V12350 Rattus norv
V2350 Rattus norv
V34963 Rattus norv
V376513 bcl.x-apopt
AJ001203 Sus scrof
AJ001203 Sus scrof
AJ01203 Sus scrof
AJ01203 Sus scrof
AJ01204 Mus musculus
U10101 Mus musculus
L135049 Mus musculus
AR060226 Eukaryoti
AR061026 Eukaryoti
AR061025 Sequence
152011 Sequence
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17349 Rattus norv
U13494 Rattus norv
U13434 Bos taurus
L14680 Rattus norv
U15645 Gallus gall
AR052621 Sequence
AR052611 Sequence
AR052618 Sequence
AR052608 Sequence
AR052608 Sequence
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AC016218 Homo sapi
AL117381 Homo sapi
D11381 Gallus gall
AR021160 Sequence
M14745 Human bcl-2
M16506 Mouse bcl-2
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D87461 Human mRNA
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U10102 Mus musculu
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AR052621
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Oy 451 tacgg 455 |||||| |Db 2062 TACGG 2066

Search completed: July 4, 2000, 01:24:21 Job time: 14809 sec

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                                              271 cccaactggggccgccttgtagcctctttctctttggggctgcactgtgtgctgagagt
                                                                                                            gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg
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GENERAL INFORMATION:
TITLE OF INVENTION: A Gene Which Prevents Programmed Cell Death
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.2%; Score 123.4; DB 6; Length 5086; 58.6%; Pred. No. 8.2e-23; tive 0; Mismatches 151; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05651
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTER STILCS:
LENGTH: 5086 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: /product= "Bcl-2" PCT-US93-05651-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
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Matches 214; Conservative
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NAME/KEY: CDS
...ATTON: 1459..2178
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PCT-US93-05651-4
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APPLICANT: Wickstrom, Eric and Rife, Jason P. TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.2%; Score 123.4; DB 6; 58.6%; Pred. No. 8.2e-23; tive 0; Mismatches 151;
                                                                                                                                                                     ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                =
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Sequence 2, Application PC/TUS9306251 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Digiplio, Frank S.
RECISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 858
                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-2
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: double
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Best Local Similarity
Matches 214; Conservat
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1762 GACGACTICTCCCGCCGCTACCGCGGCGACTICGCCGAGATGTCCAGCCAGCTGCACCTG 1821
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2002 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 2061
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                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 21.2%; Score 123.4; DB 5; Length Ebst Local Similarity 58.6%; Pred. No. 8.2e-23; Matches 214; Conservative 0; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                    APPLICANT: Reed, John TITLE OF INVENTION: Regulation of bcl-2 Gene Expression NUMBER OF INVENTIOR: 29 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEPAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-UN-1995
FRINK APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEE-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
FRIOR APPLICATION NUMBER: US 07/846,692
FRIUM DATE: 22-DEC-1988
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               Sequence 19, Application US/09080285 Patent No. 6040181
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-09-080-285-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Virginia COUNTRY: U.S.A. ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Arlington
                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                              2062 TACGG 2066
                                                 451 tacgg 455
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Pred. No. 8.2e-23;
0; Mismatches 151; Indels 0;
                        GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: human bcl-2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/365,486A FILING DATE: 23-DEC-1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 8255
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0980
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5086 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
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Best Local Similarity 58.6%;
Matches 214; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
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; LOCATION: 1459..2178
US-08-365-486A-14
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Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Read, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
                                                                                       RESULT 10
5459251-1
;PATENT NO. 5459251
; APPLICANT: TSUJIMOTO, YOSHIĞE;CTOCE, CATIO A.
TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.2%; Score 123.4; DB 7; Length 58.6%; Pred. No. 8e-23; Live 0; Mismatches 151; Indels
                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,704
FILING DATE: 18-APR-1994
PRION APPLICATION DATA:
APPLICATION NUMBER: 994,941
FILING DATE: 23-DEC-1992
APPLICATION NUMBER: 663,010
FILING DATE: 19-MAR-1991
APPLICATION NUMBER: 883,687
FILING DATE: 09-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 21.2
Best Local Similarity 58.6
Matches 214; Conservative
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451 tacgg 455
                                  604 TACGG 608
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US-08-465-485A-19
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                                                                                                                                                                                   SEQUENCES:
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                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: US-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.2%; Score 123.4; DB 3;
58.6%; Pred. No. 8.2e-23;
tive 0; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REPERBENGLY-POCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEDPHONE: (408) 436-2070
                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-5EP-1993
PRIOR APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-08-365-486A-14
: Sequence 14, Application US/08365486A
                                                                         IBM PC compatible
                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (408) 436-2075 INFORMATION FOR SEQ ID NO: 1
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Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                            OPERATING SYSTEM:
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U.S.A.
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US-08-465-485A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICAMT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                         NAME: Forthey, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/POCKET NUMBER: 3335-070-55 CONT
TELECOMUNICATION INFORMATION:
TELEPRONE: (408) 436-2070
TELEPRONE: (408) 436-2075
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                      APPLICATION NUMBER: US 07/840,716 FILING DATE: 21-FEB-1992 PRIOR APPLICATION DATA:
US 08/124,256
                                                                                   US 07/288,692
                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
            FILING DATE: 20-SEP-1993 PRIOR APPLICATION DATA:
                                                                                               FILING DATE: 22-DEC-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               LENGTH: 717 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 214; Conservative
                                                                                    APPLICATION NUMBER:
 APPLICATION NUMBER:
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US-08-465-485A-20
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Best Local Similarity
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Pred. No. 4.8e-23;
0; Mismatches 151; Indels 0;
                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
                                                                                                                                                                                                                           PRIOR APPLICATION:

APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-UNN-1995
FILING DATE: 05-UNN-1995
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY AGENT: NFORMATION:
ANNEL: DOTTON NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                           E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fortney, Andrew D. REGISTRATION NUMBER: 34,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 21.2%;
Best Local Similarity 58.6%;
Matches 214; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (408) 436-2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Virginia
                    U.S.A.
                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: 1..7
US-09-080-285-20
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                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                   22202
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                    COUNTRY:
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                                                                                                     158 togagaccogettecggegeaecttetetgatetggeggeteagetgeatgtgaeeceag 217
                                                                                                                                                                                    218 getcageccageaacgettcacccaggtctccgacgaacttttcaagggggccccaact 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    724 ACAATGCAGCAGCCGAGAGCCCGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 783
                                         Gaps
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22.5%; Score 131; DB 3; Length 926; 56.3%; Pred. No. 6e-25;
                                       0; Mismatches 190; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Vertebrate Apoptosis Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
CURRENT APPLICATION NUMBER: PC-7/USS4/07089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JMBER: PCT/US94/07089
CONCURRENTLY FILED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARCD090
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08/081.448
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REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: AR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/081
FILING DATE: 22 JUNE 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                     Matches 245; Conservative
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                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                     DB 6; Length 926;
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TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                 Score 131; DB 6; Length 92
Pred. No. 6e-25;
0; Mismatches 190; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1755 S. Jefferson Davis Hwy., Suite 400 CITY: Arlington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/08465485A; Patent No. 5831066; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-
                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                 22.5%;
ilarity 56.3%;
Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                            135..836
                                      linear
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                                                                                       ; NAME/KEY:
; LOCATION:
PCT-US94-07089-6
                                      TOPOLOGY:
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                                                                        FEATURE
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COMPUTER READABLE FORM:
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ZIP: 77210
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; LOCATION:
US-08-470-670A-6
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421 agtggggggtggggggggttcacagctctatacggggacggggcctggaggaggagggggg
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321 No. 5646008th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,448
FILING DATE: 19930622
CLASSIETTAMENT.
                                                                                                                                       Sequence 5, Application US/08081448
Patent No. 5646008
GENERAL INFORMATION:
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: No. 5646008thrup, Thomas E.
REGISTRATION NUMBER: 33,268
REGISTRACE/DOCKET NUMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
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SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 135..836
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CLASSIFICATION:
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                                                                       278 ggggccgccttgtagccttctttttggggctgcactgtgtgctgagagtgtcaaca 337
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,670A
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APPLICANT: Thompson, Craig B. B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 18
ADDRESSEE: Annold, White & Durkee
STREET: P.O. BOX 4433
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,448
FILING DATE: 22-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: 37,642
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08470670A Patent No. 5834309 Patent No. 5834309
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     518 tgctgacgggggccg 532
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                                                                                                                                                                                                                                              Length 579;
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         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
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Pred. No. 1e-124;
0; Mismatches 35;
                                                                                                   1483.0140001
                                                FILING DATE: February 11, 1997
CLASSIFICATION: 435
                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
IBM PC compatible
                                                                                                                          INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 579 base pairs TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.0%;
                                                                                                                                                                                                                                                              Matches 544; Conservative
                                                                                                                                                                                        TOPOLOGY: both
MOLECULE TYPE: cDNA
US-08-798-897-1
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Sequence 1, Application US/08978523 Patent No. 5883229

US-08-978-523-1

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            APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDER ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                     COMPUTER: ITAN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
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                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 14:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFRAX: 202-371-2540
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
                                                                                                                                                                                                         ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 544; Conservative
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MOLECULE TYPE: CDNA
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GENERAL INFORMATION:
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STRANDEDNESS:
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APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/978,523 FILING DATE: harewith CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                             ATTORNEY/ACENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Policy
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; Sequence 2, Application US/08978523
; Patent No. 5883229
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202-371-2540
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Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.
                                                                                                                                Score 567.8; DB 3;
Pred. No. 4.2e-136;
0; Mismatches 7;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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            SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                              Matches 572; Conservative
INFORMATION FOR SEQ ID NO:
                                                                               ; MOLECULE TYPE: CDNA
US-08-978-523-2
                                                                                                                                     Query Match
Best Local Similarity
                                                                  TOPOLOGY: both
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July 3, 2000, 21:17:32 ; Search time 57.05 Seconds (without alignments) 1328.331 Million cell updates/sec
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6D_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-998-853-2
US-08-998-897-1
US-08-091-448-5
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US-08-465-485A-20
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US-08-465-485A-19
US-08-365-486A-14
US-09-080-285-19
PCT-US93-05651-4
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5459251-3
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US-08-470-670A-1
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US-08-081-448-1
                                                                                                                                                                                           230463 seqs, 64992525 residues
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Listing first 45 summaries
                                          OM nucleic - nucleic search, using sw model
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Sednence Sed		tch al Similarity 98.8%; Score 567.8; DB 2; Length 579; 572; Conservative 0; Mismatches 7; Indels 0; G atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat
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0.0000000000000000000000000000000000000	BESULT 1 19-08-798-99-97-2 Sequence 2, Application US/0 Patent No. 5789201 GENERAL INFORMATION: APPLICANT: Guastella, Jo TITLE OF INVENTION: Gene TITLE OF INVENTION: Gene TITLE OF INVENTION: Homo NUMBER OF SEQUENCES: 53 CORRESPONDENCE ADDRESS: ADDRESSE: STERNE, KES STARET: 1100 New YORK CITY: Washington STATE: DC. COUNTRY: USA ZIP: 20005 COMPUTER: EDC. COMPUTER: IBM PC compa OPPRATING SYSTEM: PC-D SOFTWARE: PATENIN BATA: APPLICATION NUMBER: US, FILLING DATE: FEDENUAY CLASSIFICATION INFORMATION REGISTRATION NUMBER: 3 RETERENCE/DOCKET NUMBER: 3 REFRENCE/DOCKET NUMBER: 3 REFRENCE/DOCK	arity onserva cccagce
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 198-897-2 nnce 2, Applicat the No. 5789201 read information PELICANT: Guast TLE OF INVENTIO MBER OF SEQUENC RRESPONDENCE AD ADDRESSEE: STE STATE: JOO STATE: DC COUNTRY: USA ZIP: 20005 MRPUTER READABLE MEDIUM TYPE: F COMPUTER: IBM OPERATING SYSTE SOFTWARE: PAREI REDIUM TYPE: F COMPUTER: IBM OPERATING SYSTE SOFTWARE: PAREI REDIUM TYPE: COMPUTER: IBM OPERATING SYSTE SOFTWARE: PAREI REFERENCE/DOCKE FILLING DATE IN TELEPHONE: 202-37 TELEPHONE: COL- TELEPHONE: COL- TELEPHONE: COL- TELEPHONE: COL- TELEPHONE: COL- TELEPHONE: COL- TELEPHONE: STO- TELEPHONE: STO- TELEPHONE: STO- TELEPHONE: COL- TELEPHONE: COL- TELEPHONE: COL- TELEPHONE: STO- TELEPHONE: COL- TELEPHONE: COL- TELEPHONE: COL- TELEPHONE: STO- TELEPHONE: STO- TELEPHONE: COL- TELEPHONE: COL- TELEPHONE: STO- TELEPHONE: COL- TELEPHONE: COL- TELEPHONE: COL- TELEPHONE: STO- TELEPHONE: COL- TELEPHONE: COL- TELEPHONE: COL- TELEPHONE: STO- TYPE: NOTE STO- TYPE: COL- TYPE: COL-	h Simila 72; C ggcgac
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[ Lobase; 1 to 299]

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Sebastiani-Kabaktchis,C. and Tessier,A.

Sebastiani-Kabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F08773 299 bp mRNA EST 20-FEB-1995 HSCZBB061 normalized infant brain cDNA Homo sapiens cDNA clone (-25b06, mRNA sequence.
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Single read.
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Insert Length: 1145 Std Error: 0.00
Seq primer: (-21)M13_universal
High quality sequence stop: 339.
Location/Qualiflers
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1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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                                                                                                                                     DB 46; Length 471;
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95277534
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/sex="Female"
/tissue_type="total brain"
                                                                                                                                Score 111.2; DB 46; Length
Pred. No. 2.7e-16;
0; Mismatches 118; Indels
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="c-25b06"
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60.78;
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                                                                                                                                                                              Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                         Similarity
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                                                                                                                                     Query Match
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MEDLINE
COMMENT
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                                                  BASE COUNT
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SOURCE

Search completed: July 4, 2000, 01:06:08 Job time: 16527 sec

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/note="Organ: brain; Vector: lafmid BA, Site_1: HindIII; Site_2: NotI; sex=Female; dev_stage=3 months old; Site_2: NotI; sex=Female; dev_stage=3 months old; sloalate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, Pb.N.A.S in press" 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGCACTGTNCGTGGAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AGCGTAGACAAGGAGATGCAGGTATTGGTGAGTNGGATCGCAGCTTAGATGGCCACTTAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 agigteaacaaggagaiggaaceaciggiggacaagigeaggagiggaiggiggeciae 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 ggagatgagttcgagacccgcttccggcgcaccttctctgatctggcgctcagctgcat 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 gtgaccccaggctcagcccaggaacgcttcacccaggtctccgacgaacttttcaaggg 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggccccaactggggccgccttgtagccttctttctctttggggctgcactgtgtgctgag 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Geccaccacitrcaacrececraccecececratrcaereaccreacarccaecrecae 60
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                      DB 21; Length 299;
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18.8%; Score 109.6; DB 21; Length
Best Local Similarity 61.2%; Pred. No. 5.5e-16;
Matches 175; Conservative 0; Mismatches 111; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 ctggagacgcggctggtcgactggatccacagcagtggggctggg 433
/dev_stage="3 months old"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           W01420 437 bp mRNA EST 18-AFK-1990
Za73d06.rl Soares fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:298187 5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                    Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holan,M., Ruchada,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-Merck EST Project
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785898.
Contact: Wilson RK
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                         385 tacctggagacgcggctggtcgactggatccacagcagtgggggctggg 433
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 62.9%; Pred. No. 5.4e-17;
Matches 193; Conservative 0; Mismatches 113; Indels
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/clone_lib="Soares_fetal_lung_NbHL19W"
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/db_xref="GDB:1243109"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCL-X.;, mRNA sequence.
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128 accaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcaccttctctg 187

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Onpublished (1997)
On Apr 7, 1998 this sequence version replaced gi:3035272.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999 30-MAR-1999 1492c06.x1 NCI_CGAP_CILI Homo sapiens cDNA clone IMAGE:2116234 3' similar to gb:MI3995 PROTEIN BCL-2-BETA (HUMAN);contains TARI.t2 MER22 repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 471)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                              76 ACCTGACATCCCAGCTCCACATCACCCCAGGACAACAGCATATCAGAGCTTTGAACAGGTAG 135
                                                                                                                                                                                                                                   136 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGGCCTTTTTCTCCCTTCG 195
                                                                                                                                                                                                                                                                                                           308 gggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtgggacaagtgc 367
                                                                                                                                                                                                                                                                                                                                                              196 GCGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 255
                                                                                                                                                                                                                                                                                                                                                                                                                     368 aggaqtggatggtgtctacctggagacgcggttggtcgac-tggatccacagcagtggg 426
                                                                                188 atctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacccaggtct 247
                                                                                                                                                                                                248 ccgacgaacttttcaagggggccccaactggggccgccttgtagccttcttctctttg 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAAGCCTTGGATCCAGGAGAACGGC 315
16 AGCAAGGGTGAGGGAGGCAGGCGACGAGTTGAACTGCGGTACCGGCGGCGCATCAGTG 75
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/tissue_type="B-cell, chronic lymphotic leukemia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www-bio.llnl.gov/bbrp/image/image.html
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High quality sequence stop: 445.
Location/Qualifiers
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Unpublished (1997
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/do.xere="crannings"
//do.xere="crannings"
//dorealib="NIH_BMAP_M_S3.1"
//dorealib="NIH_BMAP_M_S3.1"
//dox_stage="27-32 days"
//dox_stage="27-32 d
determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. Seq primer: M13 Forward POLYA-NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 cageceageaegetteaceeagteteegaegaetttteaagggggeeceaaetggg 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 gggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagttcg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 agacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccaggct 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 CCGCGTATCAGAGCTTTGAGCAGGTAGTGAATGAATGAACTCTTTCGGGATGGAGTAAACTGGG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISI GTCGCATCGTGGCCTTTTTCTCCTTTGGCGGGGCACTGTGCGTGGAAACGTAGACAAGG 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 134; Indels
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                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_LIB=NIH_BMAP_M_S3.1
TAG_TISSUE=hippocampus
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                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
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                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J
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Best Local Similarity 59.5%;
Matches 197; Conservative (
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 CACCIGACGCCCITCACCGCGAGGGACGCTITGCCACGGIGGTGGAGGAACTCTTCAGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 gotggagatgagttcgagacccgcttccggcgcaccttctctgatctggcggctcagctg 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 catgigaccccaggeteageccageaaegetteaeccaggietecgaegaaettitteaa 264
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                                01-MAY-1998
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 515)
                                    AA939725 515 bp mRNA EST 01-MAY-1997292a11.r1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1344668 5' similar to gb:L31532_rna1 Mouse bcl-2 gene
                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
On Jan 19, 1998 this sequence version replaced gi:2285479.
On Jan 19, 1998 this sequence version replaced gi:2285479.
Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
Washington University School of MedicineP
Washington University School of MedicineP
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                               encoding mbcl-2-beta (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="IMAGE:1344668"
/clone_lib="Soares_thymus_2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 304.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .515
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.
The Washu-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
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                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                     house mouse.
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RESULT 12
AA939725/c
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Poustka,A., Wellenreuther,R., Mewes,H.W., Well,B. and Wiemann,S.).
EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Well,B. and
Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germanny) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No s1 sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                     999a999cccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagttcg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 gccgccttgtagccttctttttggggctgcactgtgtgctgagagtgtcaacaagg 340
                                                                                                                                                                                                                                                                                                                                                                                                                   agacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccaggct 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cagcccagcaacgcttcacccaggtctccgacgaactttttcaagggggccccaactggg 280
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                                                                                                                                                                                                                                                                                                                                                                383 GGGAGGTAATCCCCATGGCAGCAGTGAAGCAAGCGCTGAGAGAGGCTGGCGATGAGTTTG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 AACTGCGGTACCGGAGGGTTCAGTGATCTAACATCCCAGGCTTCATATAACCCCAGGGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 CAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTCGGGATGGGGGTAAACTGGG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALL14785 584 bp MRNA EST 29-DEC-1999 DKF2D547K2090_r1 547 (synonym: hfbrl) Homo sapiens cDNA clone AL134785
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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On Jul 7, 1999 this sequence version replaced gi:5866255.
Contact: Poustka A.J.
Contact: Poustka A.J.
Max-Planck-Institute for Molecular Genetics
Max-Planck-Institute for Molecular Genetics
These rase 73, 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-8413128
Email: poustke@mping-berlin-dahlem.mpg.de
                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                       Score 125.8; DB 51; Length 404;
Pred. No. 1.1e-19;
0; Mismatches 127; Indels 0;
                                                                                                                            96
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                                             TAG_LIB-UI-R-Y0
TAG_TISSUE-Eye
TAG_SEQ=CATTG"
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ilarity 61.4%;
Conservative (
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UI-M-BH2.1-apn-b-04-0-UI.s1 NIH_BMAP_M_S3.1 Mus musculus cDNA clone
UI-M-BH2.1-apn-b-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mEST@mail.nih.gov Oligo-dr track not found, Not I site shown in beginning of sequence Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP CDNA clones will be made available by the means that is soon to be determined. When NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                             98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gotcagoccagoaacgottcacccaggtctccgacgaacttttcaagggggccccaact 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 GGACAGCATATCANAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggggccgccttgtagccttctttctctttggggctgcactgtgtgctgagagtgtcaaca 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 GGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGCCACTGTGCGTGGAAAGCGTAGACA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                /clone="DKFZp547K2090"
/clone_lib="547 (synonym: hfbr1)"
/tiswue_type="brain"
/dev_stage="fetal"
/lab_nost="X1-2Dlue"
/nte="Vector: Appl; Site_1: Not1; Site_2: Sall"
145 c 173 g 116 t 6 others
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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                                                                                                                                                                                                                                                                                                            Score 119.4; DB 79; Length 584;
Pred. No. 3.7e-18;
0; Mismatches 127; Indels 0;
                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 6 (9), 791-806 (1996)
                                                              /db_xref="taxon:9606
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                            20.5%;
60.2%;
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                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 60.2
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301 443 1706
Fax: 301 443 9890
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                    source
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TITLE
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High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avonue North, Seattle, WA 98109, USA
7e1: (206) 616-3688
Fax: (206) 616-3887
Email: jWallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Seq primer: 8766
Seq primer: 8766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 455)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Reller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBACe3.6; Genomic sequence of BAC ends" 111 c 142 g 117 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HS_5062_A2_G02_SP6E_RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=638 Col=4 Row=M, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                          492 ggggaactgggcatcagtgaggacagtgctgacgggggcgtggcactgggggcctggt 551
                                                                                                                                                                                                                                      321 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGGT 380
                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-1999
Score 148.8; DB 109; Length 549;
Pred. No. 5.5e-25;
0; Mismatches 2; Indels 0;
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Pred. No. 5.9e-22;
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=638 Col=4 Row=M"
                                                                                                                                                                                                                                                                                     aactgtaggggccttttttgctagcaagtgaa 583
                                                                                                                                                                                                                                                                                                                                 381 AACTGTAGGGGCCTTGTTTGCTAGCAAGTGAA 412
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Location/Qualifiers
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AQ401160.1 GI:4412503
    25.5%;
98.7%;
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92.8%;
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                                                   Conservative
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Best Local Similarity
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ401160
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                                                 Matches 150;
    Query Match
                               Best Local
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MEDLINE
COMMENT
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SOURCE
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0; Gaps

11; Indels

0; Mismatches

Matches 141; Conservative

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432 ggcggagttcacagctctatacggggacgggccctggaggaggaggcgcgcgtctgcggga 491

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/organism="Sprague-Dauley"
/strain="Sprague-Dauley"
/db_xref="taxuon:10116"
/clone_11b="UI-R-Y0-acg-9-07-0-UI"
/clone_11b="UI-R-Y0-acg-9-07-0-UI"
/clone_11b="UI-R-Y0-acg-9-07-0-UI"
/clone_11b="bote"="UI-R-Y0-90"
/dev_stage="adult"
/note="Vector: p7730-Pac (Pharmacia) with a modified
/note="Vector: p7730-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: ECo RI; The UI-R-Y0
library is a subtracted library derived from an
individually-tagged normalized whole-eye (mins the lens)
library. The driver for the subtraction consisted of a
pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0,
UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of
UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of
3-5 nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-Y0) was constructed as follows: PCR
amplified cDNA inserts from previous library clones from
which 3' ESTS had been derived were used as a driver in
hybridization with the normalized whole-eye library in
the form of single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-Y0
library. This procedure has been previously described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: msoares@blue.weeg.ulowa.edu
oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 404)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
224 GGGGGGGTTCACAGCTCTATACGGTGACAGCCCCTGGAGGATGCGCGGGGTTCTCCGGGA 283
                                                                                               492 ggggaactgggcatcagtgaggacagtgctgacgggggcgcgtggcactgggggccctggt 551
                                                                                                                                                            284 GGGGAACTGGGCATCAGTGAGGACAGTGCTGACNGTGGCCGTGGCGCACTTGGGGCCCTTGT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI716839 404 bp mRNA EST 10-JUN-1999 UI-R-Y0-acg-g-07-0-UI.s1 UI-R-Y0 Rattus norvegicus cDNA clone UI-R-Y0-acg-g-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On May 18, 1998 this sequence version replaced gi:3136946.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
                                                                                                                                                                                                                         Research Genetics (www.resgen.com)
Seg primer: M13 Forward
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Rattus norvegicus
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High quality sequence stop: 549.
Location/Qualifiers
     /clone_lib="RPCI-11"
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                      /sex="Male"
                                                                                                                                                                                                Conservative
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                                                                                                                                                                                  Best Local Sim.
Matches 152;
                                                                                                                                                                 Query Match
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AQ665088
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used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.

TAG_LIB-NIH_BMAP_M_S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ532175 628 bp DNA GSS 18-MAY-1999
RPCI-11-352L5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-352L5,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: bbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bepac.med.buffalo.edu/ordering) or from
Research Genet cs (http://pepac.med.buffalo.edu/ordering) or from
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                      310 gctgcactgtgtgtgctgagagtgtcaacaaggagatggaaccactggtgggacaagtgcag 369
                                                                                                                                                                                                                                                                                                                                                             370 gagtggatggtggcctacctggagacgcggctggtcgactggatccacagcagtggggc 429
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 628) 2hao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
On Feb 19, 1999 this sequence version replaced gi:4145213.
Other_GSSs: RPCI-11-35215.TJ
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                                                                                                                                                                                                DB 64; Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850
781: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                Score 156.8; DB 6
Pred. No. 7.1e-27;
                                                                                                                                                                                                                                   0; Mismatches
                                                                                          TAG_TISSUE=corpus-striatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:7635052"
/db_xref="taxon:9606"
/clone="RPCI-11-352L5"
                                                                                                                           85 g
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                                                                                                          TAG_SEQ=ACGGC"
                                                                                                                                                                                             26.9%;
90.8%;
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High Throughput Sequencing Center
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Seq Primer: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 549)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                      ö
/cell_type="Lymphocytes"
/note="Vector: pBACe3", Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
RPCI11 37 g 133 t x
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126 c 190 g 118 t 10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ665088 549 bp DNA GSS 23-JUN-1999
HS_5340_B1_A06_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=916 Col=11 Row=B, genomic survey sequence.
AQ665088
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
                                                                                                                                                                                                                                                                                                                               432 ggcggagttcacagctctatacggggacggggccctggaggaggcgcggcgtctgcggga 491
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99380589
                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                      26.1%; Score 152; DB 108; Length 628; 100.0%; Pred. No. 1e-25; Live 0; Mismatches 0; Indels 0
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/clone_lib="RPC1-11 Human Male BAC Library"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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DEFINITION
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Schutz,K., de la Bastide,M., Huang,E.N., Nascimento,L., Preston,R., Shah,R., Swaby,I., Shekher,M., Spiegel,L., Vil,M.D. and McCombie,W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Vector: Lambda Zap I; Site_1: XbaI; This library was supplied by Holly Cline (Cold Spring Harbor Labs). cDNA synthesis with oligo dT Xba I (Xba I cloning site). RNA: stage 50.56 tadpoles, total brain tissue, GTC
                                                                                                                                                                                                                                                                                                                                                             AW159063 416 bp mRNA EST 05-NOV-1999 za50N02.X1 Xenopus EST library Xenopus laevis cDNA clone za50N02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                              121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                                                                                     181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
       61 aagetgaaggcagaagggttatgtetgtggagetggececgggggagggeceageagetgae 120
                                                                                                                                                                                           334 TTCTCCGATCTGGCAGCTCAGCTGCATGTGACCCCGGGCTCGGCCCAGCAACGCTTCACC 393
                                         214 AAGCTGAGGCAGAAGGGGTATGTTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressed sequence tags from Xenopus
Unpublished (1999)
Unpublished (1998)
Contact: W. Richard McCombie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 160.6; DB 71; Length 416;
Pred. No. 9.2e-28;
0; Mismatches 79; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Fax: 516 367 8884
                                                                                                                                                                                                                              /clone_lib-"Xenopus EST library"
/tissue_type-"total brain tissue"
/cell_line="W22"TGA"
/dev_stage-"tadpole"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mccombie@cshl.org
Plate: za50 row: h column: 02
Seq primer: M13 universal forward primer
High quality sequence stop: 416.
Location/Qualifiers
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/db_xref="taxon:8355"
/clone="za50h02"
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Best Local Similarity
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ORIGIN
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KEYWORDS
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0; Gaps

296 tetttetetttggggetgeaetgtgtgetgagagtgtcaacaaggagatggaaccaetgg 355

Matches 208; Conservative

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Email: mESYGmail.nih.gov

The sequence contained an oligo-dr track that was present in the oligouncleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized corpus striatum library cDNA library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH eccord will be updated accordingly when that means is determined. Seq primer: M13 Forward
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/clone="UI-W-BHI-alx-e-10-0-UI"
/clone="UI-M-BHI-alx-e-10-0-UI"
/clone="UI-M-BHI-alx-e-10-0-UI"
/clone="UI-M-BHI-BMAP_W_S2"
/dev_stage="27-32 days"
/dev_stage="27-32 days"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/la
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 431)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
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356 tgggacaagtgcaggagtggatggtggcctacctggagacgcggctggtcgactggatcc 415
                                                                416 acagcagtgggggctgggggggttcacagctctatacggggacggggccttggaggagg 475
                                                                                                                                                                                                                                                                                                                         125 AGAGCAATGCATGCTGGAATGGATTTCTAACTCTATATGGGGATGGTGCCATAGAAGAAG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                               476 cgcggcgtctgcggggaagggaactgggcatcagtgaggacagtgctgacgggggccgtgg 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 CCAGGAGGCAACGTGAGGGGAATTGGGCATCACTGAAGACTGTCTTAACTGGAGCGGTAG 244
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National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         536 cactgggggccctggtaactgtaggggccttttttgctagcaagtga 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 CTCTGGGTGCTTTGATGACAGTAGGAGCCTTGTTTGCCAGCAAGTGA 291

    431
    organism="Mus musculus"

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97044477
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AW048567.1 GI:5909096
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Fax: 301 443 9890
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ctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcaccttc 183
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="index:105667"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
I (bases 1 to 362)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                      AA596919 362 bp mRNA EST 19-SEP-1997 vo21f08.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1050567 5' similar to TR:E123735 E123735 Rl MRNA.;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996)
On Dec 18, 1996 this sequence version replaced gi:1734345.
On Dec 18, 1996 this sequence version replaced gi:1734345.
On Dec 18, 1996 this sequence version replaced gi:1734345.
On the sequence of project
Washington University School of MedicineP
Washington University School of MedicineP
Washington University School of MedicineP
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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91.1%; Pred. No. 2.6e-57;
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/organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
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Best Local Similarity 91.1
Matches 306; Conservative
   531 AGTGGGGGCT 540
                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
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Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20
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244 gtctccgacgaactttttcaagggggccccaactggggccgccttgtagccttcttctc 303
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Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                          184 tctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
On Dec 20, 1995 this sequence version replaced gi:1133576.
Contact: Smith TPL
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PO Box 166, Clay Center, NE 68933-0
Tel: 402 762 4366
Fax: 402 762 4390
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 10 row: G column: 24
Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH108"
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On May 18 Contact:		90 80	Match Cocal Similari es 391; Cons 1 atggcgacccc 	agtgggggct cagtgcacca ccgctgcacca ccgctgcacca l CCGCTGCACCA ttctctgatct
COMMENT	FEATURES	BASE COUNT	y Ma Loc hes 1	232 172 121 232 181 292 241 352 301 412 472
Description	AW258810 um74a02.y AA596919 vo21f08.r AW326901 20104 wAR AW159063 za50h02.x AW048567 UT.W-BH1- AQ53175 RPCI-11-3 AQ65088 HS_340_B AQ401160 HS_506_A AL134785 DKZP6547K AW124015 UT.W-BH2. AA939725 v292a11.r W01420 za73406.r1 AA509753 v352c0.x FO8773 HSC25661 n AL101297 t492c06.x FO8773 HSC25661 n AL180733 ub51d09.r AA509753 v452c06.r	AA991864 ua36907 AA981864 ua36907 AA816399 mg88902.r AA323521 mc57b02.x AI323521 mc57b02.x AI32364 ubo11h12.r AA458294 vq48c03.r AI323048 mj41h10.y AI32304 mj48001.y W42014 mb16904.r1 AA015184 mh33d12.r AA015184 mh33d12.r	AW24558 up09f12.x AL099352 Drosophil AL053013 Drosophil AL073013 Drosophil AL074949 Drosophil AL10709 Drosophil AAL407070 mj39b01.r AL106924 Drosophil AL106925 Drosophil	23-DEC- CDA CLO APOPTOSI ICE. CC. Wyli Bowers, Y N. Sc S, M., MCC S, M., CC
QI.	AM258810 AM259619 AW326919 AW129061 AW159063 AW0648567 AQ65175 AQ651160 AL716839 AQ651160 AL716839 AM124015 AM139725 AM939725 AM939725 AM101297 AM101297 AM18903 AM18903 AM18903 AM18903 AM18903 AM18903 AM18903 AM18903 AM18903 AM18903 AM18903	ANOS1825 AAO818675 AAO818675 AAO826399 AI3256219 AI323620 AI323048 AI323048 AAO1814 AAO15184 AAO151441	MW226585 CNS010RY CNS0091P CNS0158F CNS016R4 AAO4970 CNS016MA CNS016MA	ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS INAGE:2300906 5' similar to SW:BCLW_MOUSE P70345 RECULATOR BCL-W. [2] SW:BCLW_MOUSE; mRNA sequent and
DB	749 880 880 1109 1109 881 881 881 881 881 881 881 881 881 88	201124444441101 201124444441101 2011244444441	883 83 83 83 83 83 83 83	540 bp ano mous 5, simil W. [2] % :663179] :663179] :azoa; Cl ntia; Sc 540) ier.L., Stepre. Stoping. No. (3) no. (4) 1977. Stoping.
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Match	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	38888888888877 76444611100000		AW258810 540 bp um/4a02.y1 Sugano mous IMAGE:2300906 5' simil REGULATOR BCL-W. [2] S AW258810 G1:6631791 EST. House mouse. Whouse musculus musculus bukaryota; Metazoa; Ch Eutheria; Rodentia; Sci I (bases 1 to 540) Marra, M., Hillier, L., Underwood, K., Steptoe, Gutter, E., Kohn, S., Si Ritter, E., Kohn, S., Si Ritter, E., Kohn, S., Si Waterston, B., Swaller, T., Ritter, E., Kohn, S., Si Waterston, B., Swaller, T., Ritter, E., Kohn, S., Si Waterston, R., Suand Wilso Unpublished (1999)
Score	357.2 2288 22788 160.6 1156.8 114.6 1111.2 1	20. 44 44444 10. 44 44444 10. 444. 70. 70. 70. 70. 70. 70. 70. 70. 70. 70		
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one is available royalty-free through LLNL; contact the onsortium (info@image.llnl.gov) for further information.
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18, 1998 this sequence version replaced gi:3137956.
Marra M/WashU-NCI Mouse EST Project 1999
Ton University School of Medicine
rest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 357.2; DB 79; Length 540;
Pred. No. 2.7e-73;
0; Mismatches 38; Indels 1;
                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="IMAGE:2300906"
/clone_llb="Sugano mouse kidney mkia"
                                                                                                                                                                                     /organism="Mus musculus"
                                                                               ouseest@watson.wustl.edu
                                                                                                                                 er: custom primer used
lity sequence stop: 465.
Location/Qualifiers
                                                                                                                                                                                                /strain="C57BL"
                                                                                                                                                                                                                                                        /sex="female"
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_gss15:*
gb_gss16:*
gb_est26:*
gb_est27:*
gb_est29:*
gb_est30:*
gb_est31:*
gb_est31:*
em_est20:*
em_est21:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        em_gss11:*
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em_est23:*
em_est23:*
em_est26:*
em_est26:*
gb_est33:*
gb_est33:*
gb_est37:*
gb_est36:*
gb_est37:*
em_est27:*
em_est27:*
em_est28:*
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9D_est41:*

9D_est41:*

9D_est41:*

9D_est43:*

em_est31:*

em_est31:*

em_est34:*

em_est32:*

em_est32:*

em_est33:*

em_est46:*

em_est33:*

em_est46:*

em_est46:*

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em_est46:*

em_est31:*

em_est
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gb_gss5:*

gb_gss7:*

gb_gss7:*

gb_gss8:*

em_gss6:*

em_gss7:*

em_gss7:*

em_gss8:*

em_gss8:*

em_gss8:*

em_gss8:*

em_gss8:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH HIGHEST LEVELS IN THE TESTIS AND OVARY.

-i- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK AND BAX FOR THEIR KILLING ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).

-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).

-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
                                                                                                                                                                                                                                                                                                                                                                                ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIROS HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C, ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.

-!- SUBJUIT: FORMS HOMODIRERS AND HETEROIMERS TOGETHER WITH BCL-2, E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.

-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.

-!- ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND THE TWO CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
                                                                                                                                                                                                                          Madison D.L., Pfeiffer S.E.; "Cloning of the 3' end of rat bax-alpha and corresponding developmental down-regulation in differentiating primary, cultured
                                                                                    Han J., Sabbatini P., Perez D., Rao L., Modha D., White E.; "The BlB 19K protein blooks apoptosis by interacting with and inhibiting the p53-inducible and death-promoting Bax protein."; Genes Dev. 10:461-477(1996).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> N (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH2.
POTENTIAL.
                                                                                                                                                                                                                                                                                                 Neurosci. Lett. 220:183-186(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE, PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS0062; BH3; 1.
PROSITE; PS50062; BC12_FAMILY; 1.
PFAM; PF00452; BC1-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, 226528; CAA81299.1; --
EMBL, U59184; AAC5298.1; --
EMBL, 132098; AAA75200.1; --
EMBL, SC6111; AAC60700.1; --
EMBL, U49729; AAC26327.1; --
HSSP, P53563; IAF3.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 37-169 FROM N.A.
                                                                                                                                                                           SEQUENCE OF 75-192 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118
165
192
72
                                                                                                                                                                                                                                                                                                                                                  STRAIN-SPRAGUE-DAWLEY; MEDLINE; 95129487.
                                                   SEQUENCE FROM N.A.
                                                                     MEDLINE; 96178771.
                                                                                                                                                                                                             MEDLINE; 97147318.
                                                                                                                                                                                                                                                                                 oligodendrocytes.
                                                                                                                                                                                               TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
-i- DOMAIN: INTRACT HH3 DOMAIN IS REQUIRED BY BIK, BID, BAK AND BAX FOR THEIR KILLING ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-
APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-i- SIMILARITY: CONTAINS A BCL-2 PAMILY.
                                                                                                                                                       PPQDASTKKLSECLRRIGDELDSNM--ELQRMIADVD-T-DSPREVFFRVAADMFADGNF 105
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CESSATION OF SPERM PRODUCTION.
-!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
EIB 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
-!- ALTERNATIVE PRODUCTS: A 21 KD MEMBRANE PROTEIN ALPHA AND THE TWO
CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
                                                                                                                                                                                   33 PGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGP- 91
                                                                                                                         ς
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia;
                                                                                            Length 192;
                                                                                                                       36; Mismatches 47; Indels
L -> M (IN REF. 2).
C -> Y (IN REF. 2).
L -> F (IN REF. 3).
D -> E (IN REF. 1).
7B3CD198D56DF589 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
                                                                                                         Pred. No. 4.44e-25;
                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                     192 AA
                                                                                         Score 231;
76 76 C
126 126 C
149 149 L
159 159 D
192 AA; 21350 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L22472; AAA03622.1; -. HSSP; P53563; 1AF3.
                                                                                        Query Match
Best Local Similarity 27.3%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    BAXA_MOUSE
                                                                                                                                                                                                                                                                                                         152 G 152
                                                                                                                                                                                                                                                                           166 G 166
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAFVELYGESARPLEDESWLSLKTLLSLALVGACIFLGAYL
GHK -> VGACLVE (IN ISOFORM BCL-2-BETA).
AA85EF6B0766BE0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 VATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREVENTING THE RELEASE OF CYTOCHROME C. MICHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
                                                                                                                                                   -:- SUBCELLULAR LOCATION. MITOCHONRIAL INNER AND OUTER MEMBRANES, AS WELL AS UNCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
-:- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
-:- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-:- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87
                                                                       SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND BAK PROTELNS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX REQUIRES INTACT BH1 AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM: PF00452; BC1-2; 1. Apoptosis; Alternative splicing; Transmembrane; Mitochondrion.
BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 236;
                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 7.73e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH2.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50062; BCL2_FAMILY; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01259; BH2; 1. PROSITE; PS01259; BH3; 1. PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L31532; AAA37282.1; -.
EMBL; M16506; AAA37282.1; JOINED.
EMBL; M16506; AAA37281.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 AA; 26425 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 45.2%;
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A25960; TVMSA1.
PIR; B25960; TVMSB1.
PIR; E37332; E37332.
HSSP; Q07817; 1MAZ.
MGD; MGI:88138; BCLZ.
                                                                                                                                                                                                                                                                                                FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptos
DOMAIN
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    셤
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 GINWGRIVAFFSFGRALCVESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 GEGATQGIVEEEVLQALLEATEEFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRD 105
                                                                                                                                                                                                                                                                                                                           -1. FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
-1. SUBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).
-1. DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
-1. SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-1. SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-1. SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.7%; Score 554; DB 1; Length 204;
47.4%; Pred. No. 6.05e-96;
7ative 28; Mismatches 51; Indels 1; Gaps
                                                                                                                                                                                                                                                            Cruz-Reyes J., Tata J.R.; "Cloning, characterization and expression of two Xenopus bcl-2-like
                                                                                      APOPTOSIS REGULATOR R11 (XR11).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Butrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 AA; 23379 MW; 3BFC6BE6DDA4CA03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAXA_RAT STANDARD; PRT; 192 AA. 063600; 062995; 064383; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-FEB-2000 (Rel. 39, Last annotation update) APOPTOSIS REGULATOR BAX, MEMBRANE ISOFORM ALPHA.
                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 LYGDGALEEARRLREG-NWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 LYGKNAAAQSRESQERFGRLLTIVMLTGVFAL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
PFAM; PF00452; BCL 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X82461; CAA57844.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 47.4%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norveqicus (Rat).
 STANDARD;
                                                                                                                                                                                                                                                                                               cell-survival genes.";
Gene 158:171-179(1995)
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          MEDLINE; 95331613.
                                                                                                                                                                                                                           TISSUE=HEAD
AR11_XENLA
091828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                      xenobns.
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   SEPTTE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                               -1- FUNCTION: PROLÒNGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE PRESENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPAGES BY PREVENTING THE RELEAGE OF CYTOCHROME C. MIGHT FUNCTION IN AN ANTICXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL) (ALSO KNOWN AS TYPE II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION T(14;18)(Q32;Q21) WHICH INVOLVES BCL2 AND IMMUNOGLOBULIN GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLUIAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
-1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE
                                                                           Hockenbery D., Nunez G., Milliman C., Schreiber R.D., Korsmeyer S.J., *Bcl-2 is an inner mitochondrial membrane protein that blocks
                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
                                                                                                                                                                                                                                                                                                                                                                                                                              BAK PROTEINS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX REQUIRES INTACT BHI AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL ENDS.
TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane; Mitochondrion; Chromosomal translocation; Polymorphism;
                                                                                                                                                                                  MEDLINE; 94239528.
Yin X.-M., Oltvai Z.N., Korsmeyer J.;
"BH1 and BH2 domains of Bcl-2 are required for inhibition of apoptosis and heterodimerization with Bax.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA35591.1; ALT_SEQ.
AAA35591.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD14111.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , PSO1080; BH1; 1.
; PSO1258; BH2; 1.
; PSO1259; BH3; 1.
; PSO1260; BH4_1; 1.
                                                                                                                           Nature 348:334-336(1990)
                                                                                                                                                                                                                                                             Nature 369:321-323(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAA29778.
 Blood 79:229-237(1992).
                                                                                                                programmed cell death.
                                  SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A24428; TVHUBC.
C37332; C37332.
D37332; D37332.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A29409; TVHUA1
B29409; TVHUB1
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                                                        MEDLINE; 91066924
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                                                                                                                                                                      MUTAGENESIS
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HSSP;
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PIR;
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PIR;
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                                                                                           GHK -> VGASGDVS (IN ISOFORM BCL-2-BETA).
G->A: NO HETERODIMERIZATION WITH BAX, AND
                                                                              DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
                                                                                                                                                                                                             /FTId=VAR_000828.
V -> I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
                                                                                                                                                                                      P -> S (IN NON-HODGKINS-LYMPHOMA; SOMATIC
                                                                                                                                                                                                                                                                                                                                                                                                 81 AAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELFRD 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/C; TISSUE-LIVER; MEDLINE; 87187643.
Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.; Modrular analysis of mbci-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eguchi Y., Ewert D.L., Tsujimoto Y.; "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in
                                                                                                                                                                                                                                                                                                                                                                         5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adult and embryo.";
Nucleic Acids Res. 20:4187-4192(1992).
-!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS
                                                                                                                   LOSS OF ANTI-APOPTOTIC ACTIVITY. W->A: NO HETERODIMERIZATION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                               LOSS OF ANTI-APOPTOTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                               Length 239;
                                                                                                                                                                                                                                                                                                                                                                        44; Mismatches 41; Indels
                                                                                                                                                                                                                                                                I -> F (IN REF. 4).
P -> T (IN REF. 3).
S -> R (IN REF. 3).
R -> C (IN REF. 4).
A; 3C49F2B714DC9CCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 LYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 2.68e-103;
                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                     /FTIG=VAR_000829
                                                                                                                                                                     /FTId=VAR_000827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p10417; P10418;
01.MAR-1989 (Rel. 10, Created)
01.APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 236 AA.
                                                                                                                                                                                                                                                                                                                                               Score 586;
                                                                                                                                                                                                                                         MUTATION)
                                                                                                                                                                                                  MUTATION
                                                                                                                                                                                                                                                                48 I
59 P
117 S
129 R
26266 MW;
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Local Similarity 45.1%;
                                                                                                                                                                                                                                                                                                                                                                         74; Conservative
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107
155
202
233
233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                   239 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92375724.
 Disease mutation,
                        93
136
187
212
196
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                                                                                                                                                                                                                                                                             CONFLICT
                                                               FRANSMEM
                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                   CONFLICT
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                                                                                                       MUTAGEN
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           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: TITOCHONDRIAL INNER AND OUTER MEMBRANES, AS WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
-1- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THERE C-TERMINAL ENDS.
-1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES, WITH HIGHEST LEVELS IN REPRODUCTIVE TISSUES. IN THE ADULT BRAIN, EXPRESSION IS LOCALIZED IN MITRAL CELLS OF THE OLFACTORY BULL, GERBELLAR GRANULE NEURONS OF HIPPOCAMPUS, PONTINE NUCLEI, GRANULE AND PYRAMIDAL NEURONS OF HIPPOCAMPUS, PONTINE NUCLEI, GERBELLAR GRANULE NEURONS, AND IN BPENDYMAL CELLS. IN PRENATAL BRAIN, EXPRESSION IS HIGHER AND LOCALIZED IN THE NEUROEPITHELIUM AND IN THE CORFICAL PLATE.
-1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                         adult rat brain.";
Neuroscience 61:165-177(1994).
-!- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF
VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS
BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY
PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN
ANTIOXIDANT PARHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL
GENERATION SUCH AS MITOCHONDRIA.
                                                                                                                          "Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorinoric gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xiong messenger ribonucieic acid levels."; Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAK PROTEINS, AND WITH BCL-X(S). HETERODIMERIZATION WITH BAX REQUIRES INTACT BHI AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                   "bcl-2 messenger RNA is localized in neurons of the developing and
                                                                                                                                                                                                                                                                                                                                       MEDLINE; 95059917.
Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROMINE, PEO0452; BC1-2; 1.
Apoptosis; Alternative splicing; Transmembrane; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-:- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-:- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-:- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-:- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                      STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY; MEDLINE; 95129487.
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PROSITE; P550062; BCL2_FAMILY; 1.
PROSITE; P501080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
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                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 19-172 FROM N.A.
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152
     Gene 140:291-292(1994)
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                                                                                                                                                                                                                                                                                                                                                                                              Lindholm D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE: 87002488.
Cleary M.L., Smith S.D., Sklar J.;
Cleary M.L., Smith S.D., sklar J.;
"Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2.
2.immunoglobulin transcript resulting from the t(14;18)
translocation.":
                                                                                                                                                                                                                                                                                           76 VANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
                                                                                                                                                                                                                                                                                                                                                                                     136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
                                                                                                                                                                                                                                                                                                                                                                                                                    5; Gaps
                                                                                                                                                                                                                                                                                                                             28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-Ig fusion gene in lymphoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tsujimoto Y., Croce C.M.; "Analysis of the structure, transcripts, and protein products of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-131 FROM N.A., AND VARIANTS NON-HODGKINS-LYMPHOMA. MEDLINE; 92096610.
Tanaka S., Loule D.C., Kant J.A., Reed J.C.;
"Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-Hodgkin's lymphomas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,
                                                                                                                                                                                            Length 236;
                                                                                                                                                                                                                                          43; Mismatches 43; Indels
                                              A -> R (IN REF. 2).
E -> G (IN REF. 1).
S -> Y (IN REF. 2).
L -> O (IN REF. 2).
H; E7688CB9071A872A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bcl-2, the gene involved in human follicular lymphoma.";
proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 586; DB 1; Losted. No. 2.68e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCL2_HUMAN STANDARD; PRT; 239 AA. P10415; P10416; Q16197; Q13842; Q1-MAR-1989 (Rel. 10, Created) O1-APR-1993 (Rel. 25, Last sequence update) APOPTOSIS REGULATOR BCL-2.
  BH2.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 20:4187-4192(1992).
199 BH
230 PC
42 A
157 E
167 S
212 L
26622 MW;
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                                                                                                                                                                                            41.9%;
                                                                                                                                                                                                                        Best Local Similarity 45.2%;
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBO J. 7:123-131(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell 47:19-28(1986).
                                                                                                                      212
236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 92375724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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  DOMAIN
TRANSMEM
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CONFLICT
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SEQUENCE
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                                                                                                                                                                                                 Query Match
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Cazals-Hatem D.L., Loule D.C., Tanaka S., Reed J.C.;

"Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue of the Bcl-2 encoprotein."; publication of the Belochim. Blophys. Acta 113:109-113(1992).

-!- FUNCTION: PROLONGS THE SIRVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STAMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS BECARGE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY PREVENTING THE RELEASE OF CYTCHROME C. MIGHT FUNCTION IN AN ANTIOXIDANT PARHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA (BY SIMILARITY).

-!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND BAX PROTEINS. HETERODIMERIZATION WITH BAX REQUIRES INTACT BHI AND SUCH AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARIAND SUCH AND SUCH
                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                          FSRK -> VRTTPLVCPPLACVSLLCEHP (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                       MISSING (IN ISOFORM BCL-X(S)).
DTFVDLYGNNAAAESRKGQERFNRWFLIGMTVAGVVLLGSI
                                                                                                                                                                           LYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRK
-> GHDCGWCGSAGLTLQSEVTRH (IN ISOFORM BCL-
                                                                                                                                                                                                                                                                                                                                                                                             85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                                                                            101 LFGAALCAESVUKEMEPLVGQVQEMMVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92375724.

Eguchi Y., Ewert D.L., Tsujimoto Y.;

"Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                 DB 1; Length 233;
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                                                                                                                                                                                                                                                                                                                                                  30; Mismatches 36; Indels
                                                                                                                                                                                                                                                24D2AC79887E072E CRC64;
                                                                                                                                                                                                                                                                                                 Score 615; DB 1; LA Pred. No. 5.42e-110;
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 AA.
                                                                                                                                                                                                                            X(DELTA-TM))
                                                                                                                                               BCL-X-BETA)
                                                     POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 RLREG-N-WASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                26132 MW;
                                                                                                                                                                                                                                                                                                 44.08;
53.18;
                                                                                                                                                                                                                                                                                                                     Best Local Similarity 53.1%;
Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCL2 OR BCL-2.
Gallus gallus (Chicken).
  148
195
226
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233
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  129
180
210
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                                           TRANSMEM
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SIMILARITY). -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES. -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC

SIMILARITY)

-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 PNWGRLVAFFLEGAALCAESVNKEMEPLVGQVQEMWVAYLETRLVDWIHSSGGWAEFTAL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 PAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVEELFRDG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 VNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGWDAFVEL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BRAIN;
BUDLINE; 94193015.
Sato T., Irie S., Krajewski S., Reed J.C.;
"Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E -> S (IN REF. 2).
GSAAASEVPPAEGLRP -> ARLLLVRCPRLRGCA
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 233;
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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H -> T (IN REF. 2).
G -> V (IN REF. 2).
5252555ACB6E4C3D CRC64;
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Pred. No. 1.57e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Mismatches
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EMBL; D11381; BAA01978.1; JOINED.
EMBL; Z11961; CAA78018.1; -.
PIR; A37332; A37332.
PIR; S24390; S24390.
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PROSITE: PS50062; BCL2_PAMILY: 1.
PROSITE: PS01080; BH1; 1.
PROSITE: PS01258; BH2; 1.
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PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
PFAM; PF00452; BC1-2; 1.
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Best Local Similarity 46.6%;
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181
208
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                                                                                                                                                               MISSING (IN ISOPORM BCL-X(S)).
DTFVDLYGNNAAAESRKGGERFNRWELTGMTVAGVVLLGSL
FSRK -> VRTTPLVCPPLVCLSSVEIPNCFWSPGNVED
IDYSGDIPGLL (IN ISOFORM BCL-X(BETA)).
R -> Q (IN REF. 1).
R -> G (IN REF. 2).
A -> E (IN REF. 2).
A -> E (IN REF. 4).
FF -> SS (IN REF. 4).
A -> V (IN REF. 4).
A -> T (IN REF. 4).
A -> T (IN REF. 4).
A -> P (IN REF. 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
               PFAM; PF00452; BC1-2; I. Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Mammalia,
Eutheria; Rodentia, Sciurognathi; Muridae; Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thompson C.B., Nunez G.; RRNA form expressed during murine "bc! XI is the major bc!-x mRNA form expressed during murine development and its product localizes to mitochondria."; bevelopment 120:3033-3042(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                        44.0%; Score 615; DB 1; Length 233 larity 53.1%; Pred. No. 5.42e-110; Conservative 30; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (X(L); X(S) AND X(DELTA-TM) ISOFORMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCLX_MOUSE STANDARD; PRT; 233 AA. 064373; 060657; 060658; 061338; 01-NOV-1997 (Rel. 35, Created) PLINOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS).
STRAIN-C57BL/6; TISSUE=BRAIN;
MEDLINE; 95331139.
                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::| | | ::| | | 11:|
161 RLREG-N-WASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lymphocytes.";
J. Immunol. 153:4388-4398(1994).
                                                                                                                                                                                                                                                                                                                                                                                201 A
26158 MW;
 PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APOPTOSIS REGULATOR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                           119
144
199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                         119
143
199
201
233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 95052604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   64
64
81
                                                       3D-structure.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=2A4B;
                                                                                                                                                                                                                                               CONFLICT
CONFLICT
CONFLICT
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                   DOMAIN
TRANSMEM
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                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                             CONFLICT
 PROSITE;
                                                                                               DOMAIN
                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: BCL-X(BETA)IS EXPRESSED IN BOTH EMBRYONAL AND POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN POSTNATAL TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                    Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N., Ohta S., Seldin M.F., Nunez G.;

"Genomic organization, prometer region analysis, and chromosome localization of the mouse bcl-x gene.";

J. Immunol. 158:4750-4757(1997).

-!- FUNCTION. DOMINANT REGULATION OF APOPTOTIC CELL DEATH. THE LONG FORM AND THE DELTA-TH FORM DISPLAY CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).

-!- SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAX, WHEREAS BCL-X(S) FORMS HETERODIMERS WITH BAX AND BAX, WHEREAS BCL-X(S) FORMS HETERODIMERS WITH BAX AND BAX, WHEREAS BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).
ALTERNATIVE PRODUCTS: FOUR ISOFORMS, BCX-X(L) (SHOWN HERE), BCL-X(S), BCL-X-BETA AND BCL-X(DELTA-TM), ARE DERIVED BY ALTERNATIVE PLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL.X(L) AND BCL.X(DELTATM) EXPRESSION IS ENHANCED IN B AND I LYMPHOCYTES THAT HAVE BEEN ACTIVATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: BH ADMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).

SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).

SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                       Yang X.-F., Weber G.F., Cantor H.; A novel Bol.x isoform connected to the T cells "receptor regulates apoptosis in T cells." Immunity 7:629-639(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis; Mitochondrion; Alternative splicing; Transmembrane. DOMAIN 4 24 BH4. DOMAIN 86 100 BH3.
                                                               STRAIN-C57BL/6 X CBA; TISSUE-THYMUS;
MEDLINE; 98051053.
[4]
SEQUENCE FROM N.A. (BETA ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U78031; AAB96881.1; -.
EMBL; U78030; AAB96881.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X83574; CAA58557.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U10101; AAA82173.1; --
EMBL; U10100; AAA82173.1; --
EMBL; U51279; AAC53460.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L35049; AAA51039.1; -. EMBL; L35048; AAA51040.1; -.
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PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
PFAM; PF00452; BC1-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:88139; BCL2L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1AF3
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                                                                                                                                                                                                                                                                                      [5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 97289584.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P53563;
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                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
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SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 FFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWERFVDLYGNNAAAE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (BY SIMILARITY).
-!- ALTERNATIVE PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT ISOFORM ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
                                                                                                                                                            DEVELOPMENT.

-1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).

-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).

-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).

-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).

-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).

-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSRK -> VRTALP (IN SHORT ISOFORM) 229 AA; 25733 MW; A97D3A4D04C0E9DA CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 615; DB 1; Length 229;
Pred. No. 5.42e-110;
30; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BCLX_RAT STANDARD; PRT; 233 AA.
P53563; Q62678; P70614; P70613; Q62836; Q64087; Q64128; Q1-00T-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
APOPTOSIS REGULATOR BCL-X.
BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis; Transmembrane; Alternative splicing.
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POTENTIAL.
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EMBL, U26645, AA807677.1; --
FIR, A47537, A47537.
HSSP, P53563, 1AF3.
PROSITE; P530062; BCL2_FAMILX; 1.
PROSITE; P501080; BH1; 1.
PROSITE; P501259; BH3; 1.
PROSITE; P501259; BH3; 1.
PROSITE; P501259; BH4, 1, 1.
PROSITE; P501259; BH4, 1, 1.
PROSITE; P501259; BH4, 1, 1.
PROSITE; P501263; BH4_1; 1.
PROSITE; P501263; BH4_1; 1.
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llarity 52.3%;
Conservative
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223
229
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nes 78; Conserv
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                                                                                                                                                                                                                                                                    Ohta S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENVELOPE (BY SIMILARITY).

-I-ALTERNATIVE PRODUCTS: THREE ISOFORMS, BCL-X(L) (SHOWN HERE),
BCL-X(S) AND BCL-X(BETA), ARE DERIVED BY ALTERNATIVE SPLICING.

-I-TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wesselingh S.L., David G.L., Choi S., Veliuona M., Hardwick J.M.; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
                                                                                                                                                   MEDLINE; 96278736.
Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Oh
"An additional form of rat Bcl.x, Bcl.xbeta, generated by an
unspliced RNA, promotes apoptosis in promyeloid cells.";
J. Biol. Chem. 271:13258-13265(1996).
                                   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS). STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY;
                                                                                                                             SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S76513; AAC60701.1; ALT_INIT.
S78284; AAC60702.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50062; BCL2_FAMILY; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS01259; BH3; 1. PROSITE; PS01260; BH4_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X82537; CAA57886.1; -.
EMBL, X82537; CAA57887.1; -.
EMBL, U10579; AAA19257.1; -.
EMBL, U7250; AAB17353.1; -.
EMBL, U7249; AAB17352.1; -.
                                                                                                                                                                                                                                                            MEDLINE; 95129487.
                                                              SEQUENCE FROM N.A.
                        Michaelidis T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY)
                                                                                                                                           TISSUE-THYMUS
                                                                          TISSUE-BRAIN;
            ISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1AF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C. INALURE 381.335-341(1996).

NATURE 381.335-341(1996).

PORM DISPLAYE CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT ISOFORM PROMOTES APOPTOSIS.

C. ISOBUNIT: BCL.X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS EDGLAYE, SPERM TO BE REQUIRED FOR AWIL-APOPTOTIC ACTIVITY.

C. ISOBCLIAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPEE (BY SIMILARITY).

C. ISOBCLIAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPEE (BY SIMILARITY).

C. ISOBCLIAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPEE (BY SIMILARITY).

C. ISOBCLIAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPEE (BY SIMILARITY).

C. ISOBCLIAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPER (BY SIMILARITY).

C. ISOBCLIAR LOCATION: MITOCHONDRIAL MEMBRANES AND SECULOR SECONTAINING LYMPHOCYTES. IN CONTRAST, BCL.X(L) IS FOUND IN TISSUES CONTAINING LYMPHOCYTES. IN CONTRAST, BCL.X(L) IS FOUND IN TISSUES CONTAINING LYMPICALLY BHI AND BELL DOMAINS ARE REQUIRED FOR ANTI-APOPTOTIC CELLS, SUCH AS ADDLY BRAIN.

C. ISOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC CHUSTNING AND ADDLY BRAIN AND AND ADDLY BRAIN.

C. ISOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC CHUSTNING AND ADDLY BRAIN.
           Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B., Korsmeyer S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 96256675.

Muchanore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
Yoon H.S., Nettesheim D., Chang B.S., Thompson C.B., Wong S.L.,
Ng S.L., Reslat S.W.;
X.ray and NMR structure of human Bcl-xL, an inhibitor of programmed cell death.";
                                                                                                                                                                    MEDLINE; 96170038.
Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
Korsmeyer S.J.;
                                      Korsmeyer S.J.;
Multiple Bcl-2 family members demonstrate selective dimerizations
                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 1-209.
MEDILES, 97172562.
Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,
Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
Thompson C.B., Fesik S.W.;
"Structure of Bel-x-Bak peptide complex: recognition between regulators of apoptosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                  "Bax-independent inhibition of apoptosis by Bcl-XL.";
Nature 379:554-556(1996).
                                                                                               Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995)
                                                                                                                                             JUTAGENESIS OF BH1 AND BH2 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z23116; CAA80662.1; -. EMBL; Z23115; CAA80661.1; -. EMBL; U72398; AAB17354.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH1; 1.
BH2; 1.
BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 275:983-986(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1MAZ; 21-APR-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1BXL; 29-OCT-97
1LXL; 21-APR-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01080;
PROSITE; PS01258;
PROSITE; PS01259;
MEDLINE; 95372373.
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                                                                                      with Bax
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Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus
                                                                                                                                                                                                                                                                  DTFVELYGNNAAAESRKGGERFNRWFLTGMTVAGVVLLGSL
FSRK -> VRTKPLVCPFSLASGSRSTFALLLLLLLLLCWVI
VGDUDS (IN ISOFORM BCL-X(BETA)).
FRD->VRA: NO HETERODIMERIZATION WITH BAX.
VNW->AIL: LOSS OF ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REDUCES ANTI-APOPTOTIC ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 93364977.

Bolse L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T., Turka L.H., Gonzalez-Garcia M., Thompson C.B.;

"bcl.x, Mao X., Nunez G., Thompson C.B.;

"bcl.x, a bcl.2-related gene that functions as a dominant regulator of apoptotic cell death.";

cell 74:597-608(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Reprod. Dev. 47:26-29(1997).
-i- FUNCTION: DOMINANT REGULARON OF APOPTOTIC CELL DEATH. THE LONG
FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVITY.
G->A: NO HETERODIMERIZATION WITH BAX.
G->E: NO HETERODIMERIZATION WITH BAX.
                                 PFAM; PF00452; Bcl-2; 1. Apptosis; Mitochondrion; Alternative splicing; Transmembrane; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                       GRI->ELN: LOSS OF ANTI-APOPTOTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vilagrasa X., Mezquita C., Mezquita J.; "Differential expression of bcl-2 and bcl-x during chicken spermatogenesis.";
                                                                                                                                                                                                                                             MISSING (IN ISOFORM BCL-X(S))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 616; DB 1; Length 233;
Pred. No. 3.18e-110;
30; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G -> A (IN CAA80661).
E09D3CDD851AE9BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       007816; 098908;
01-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BCL2L1 OR BCLX OR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (LONG FORM).
STRAIN-HUBBARD WHITE MOUNTAIN; TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY ABOUT HALF
                                                                                                                                                                                                                              POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::| | | ::| | | ::| | | ::| 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (SHORT FORM). MEDLINE; 93364977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26049 MW;
PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 44.1%;
Local Similarity 53.1%;
Les 77; Conservative
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148
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100
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195
226
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148
188
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TRANSMEM
VARSPLIC
VARSPLIC
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DOMAIN
DOMAIN
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                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myocardium of pig.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DOWINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 LETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 SRALVEDLVRYKLCQRSLV - PEPS-GAASCALHSAMRAAGDEFEERFRQAFSEISTQIH 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.,
"Expression of apoptosis-associated genes in hibernating and stunned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE BETA ISOFORMS PROMOTE APOPTOSIS.
SUBUNIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS
BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (BY SIMILARITY).

DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 931; DB 1; Length 228; Pred. No. 3.73e-184;
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 AA; 25068 MW; C499D449A585F8A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BCLZLI OR BLCZL OR BCLX.
                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01080; BH1; 1.
PROSITE; PS01058; BH2; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
PFAM; PF00452; BCL-2; 1.
                                                                                                                                                                                                                                                                                            EMBL; X82462; CAA57845.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Apoptosis; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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077737;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVLNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T., Turka L.A., Mao X., Nunez G., Thompson C.B.;
"bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptoric cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 233;
APOPTOTIC ACTIVITY (BY SIMILARITY).

-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).

-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).

-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).

-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).

-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inohara N., Ohta S.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 100 BH3.
129 148 BH1.
180 195 BH2.
210 226 POTENTIAL.
233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 618; DB 1; Lo
Pred. No. 1.10e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        007817; 092976;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
PROSITE; PS0063; BH4_2; 1.
PROSITE; PS0063; BH4_2; 1.
PROMITE; PS00452; BH4_2; 1.
Apoptosis; Mitochondrion; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 KGQERFNRWFLTGMTLAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 RLREG-N-WASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (BETA ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ001203; CAA04597.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 44.2%;
Local Similarity 53.8%;
es 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APOPTOSIS REGULATOR BCL-X. BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 93364977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCLX_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                     1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                             Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                   9 29 BH4.
85 104 BH1.
136 151 BH2.
193 AA; 20774 MW; 3792243A50281761 CRC64;
                                                                                                                                                                                                                                                                                                             Score 1383; DB 1; Pred. No. 2.09e-292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                    PROSITE; PS50062; BCL2_FAMILY; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS01260; BH4_1; 1. PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1. PFAM; PF00452; BC1-2; 1.
                   EMBL; U59747; AAB09055.1; -. EMBL; D87461; BAA19666.1; -.
                                                                                                                                                                                                                                                                                                                                191; Conservative
                                                                                                                                                                                                                                                                                                               99.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APOPTOSIS REGULATOR BCL-W. BCL2L2 OR BCLW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND SALIVARY GLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D87461; BAA196
HSSP; P53563; 1AF3.
MIM; 601931; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 96358615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 2
BCLW_MOUSE
P70345;
                                                                                                                                                                                                   Apoptosis.
DOMAIN
                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                             DOMAIN
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                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MATPASTPDIRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olivov-1997 (Rel. 35, Created)
Ol-NOV-1997 (Rel. 35, Last sequence update)
Ol-NOV-1997 (Rel. 35, Last annotation update)
APOPTOSIS REGULATOR RI (XRI) (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 193;
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 29 BH4.
85 104 BH1.
136 151 BH2.
193 AA, 20790 MW, 36CA185F5945DFB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1380; DB 1;
Pred. No. 1.10e-291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                      MGD; MGI:108052; BCL212.
PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01268; BH4, 1; 1.
PROSITE; PS50063; BH4, 2; 1.
PROM; PF00452; BC1-2; 1.
                                                                                                                                                                                                                                                               EMBL; AF030769; AAB86430.1;
HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 97.9%;
Matches 189; Conservative
                                                                                                                                                                                                                                         EMBL; U59746; AAB09056.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=HEAD;
MEDLINE; 95331613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apoptosis.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR1_XENLA
Q91827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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protein · protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Jun 23 14:14:40 2000; MasPar time 7.84 Seconds 749.617 Million cell updates/sec Run on:

Tabular output not generated

>US-09-155-327B-7 (1-193) from US09155327B.pep 1397 Description: Perfect Score:

1 MATPASAPDTRALVADFVGY......LTGAVALGALVTVGAFFASK 193 PAM 150 Gap 11 Scoring table: Sequence:

83857 segs, 30454973 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

1:swissprot swiss-prot38 Database:

Mean 46.104; Variance 80.361; scale 0.574 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	2.09e-292	1.10e-291	3.73e-184	1,10e-110	3.18e-110	5.42e-110	5.42e-110	5.42e-110	1.57e-103	2.68e-103	2.68e-103	7.73e-103	6.05e-96	4.44e-25	4.44e-25	1.12e-24	1.78e-24	1.78e-24	4.50e-24	7.14e-24	1.79e-22	6.86e-21	1.15e-15
	i	B	R	Z	B	BC	ည္ထ	BC	BC	ВС	BC	BC	R	R1	BA	BA	BA	NSW	BA	AG	AG	BA	JAG.	Ä
	uo	REGULATOR	REGULATOR	REGULATOR	REGULATOR	REGULATOR	REGULATOR	REGULATOR	REGULATOR	REGULATOR	REGULATOR	REGULATOR	REGULATOR	REGULATOR	REGULATOR	REGULATOR	REGULATOR	BAX PROTEIN, CYTOPLASM	APOPTOSIS REGULATOR	BCL-2 HOMOLOGOUS ANTAG	HOMOLOGOUS ANTAG	APOPTOSIS REGULATOR BA	BCL-2 HOMOLOGOUS ANTAG	APOPTOSIS REGULATOR
	Description	APOPTOSIS	APOPTOSIS	APOPTOSIS	APOPTOSIS	APOPTOSIS	APOPTOSIS	APOPTOSIS	APOPTOSIS	APOPTOSIS	APOPTOSIS	APOPTOSIS	APOPTOSIS	APOPTOSIS	APOPTOSIS	APOPTOSIS	APOPTOSIS	BAX PROTE	APOPTOSIS	BCL-2 HOM	BCL-2 HOM	APOPTOSIS	BCL-2 HOM	APOPTOSIS
	an T	BCLW_HUMAN	BCLW_MOUSE	AR1_XENLA	BCLX_PIG	BCLX_HUMAN	BCLX_CHICK	BCLX_RAT	BCLX_MOUSE	BCL2_CHICK	BCL2_RAT	BCL2_HUMAN	BCL2_MOUSE	AR11_XENLA	BAXA_RAT	BAXA_MOUSE	BAXA_BOVIN	BAXD_HUMAN	BAXA_HUMAN	BAK_HUMAN	BAK2_HUMAN	BAXB_HUMAN	BAK_MOUSE	NR13_COTJA
	BB :	Н	Н	Н	Н	٦	Н	٦	Н	-	, ,	-1	~	ч	H	Н	~4	-1	Н	, ,	Н	-	-	7
:	Match Length DB	193	193	228	233	233	229	233	233	233	236	239	236	204	192	192	192	143	192	211	211	218	208	177
Query	Match	99.0	98.8	9.99	44.2	44.1	44.0	44.0	44.0	42.0	41.9	41.9	41.8	39.7	16.5	16.5	16.4	16.3	16.3	16.2	16.1	15.6	15.0	13.1
	Score	1383	1380	931	618	616	615	615	615	587	586	286	584	554	231	231	229	228	228	226	225	218	210	183
Result	. : Q	1	7	e	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

1.11e-10	1.68e-10	1.95e - 09	1.30e-09	2.93e-09	2.38e-06	3.49e-06	3.49e-06	2.93e-01	7.61e-01	1.42e+00	1.04e+00	1.42e+00	1.04e+00	1.04e+00	1.04e+00	1.93e+00	1.93e+00	1.93e+00	1.93e+00	1.93e+00	1.93e+00
APOPTOSIS REGULATOR CE	BCL2-RELATED PROTEIN A	BCL2-RELATED PROTEIN A	INDUCED MYELOID LEUKEM	APOPTOSIS REGULATOR CE	APOPTOSIS REGULATOR BC	APOPTOSIS REGULATOR BC	APOPTOSIS REGULATOR BC	NODULATION PROTEIN NOL	HYPOTHETICAL 67.1 KD P	LIGNINASE C PRECURSOR	GLUCAN 1, 3-BETA-GLUCOS	DNA-DAMAGE-INDUCIBLE P	GAG POLYPROTEIN [CONTA	PROBABLE ABC TRANSPORT	LOW-DENSITY LIPOPROTEI	HYPOTHETICAL 36.5 KD P	L-ARABINOSE ISOMERASE	MYOCYTE-SPECIFIC ENHAN	COMPETENCE PROTEIN COM	PULLULANASE PRECURSOR	PUTATIVE HELICASE HELY
CED9_CAEBR	BFL1_MOUSE	BFL1_HUMAN	MCL1_HUMAN	CED9_CAEEL	EAR_ASFE4	EAR_ASFM2	EAR_ASFB7	NOLO_RHISN	YH70_SYNY3	LIGC_TRAVE	EXG_YARLI	DINF_ECOLI	GAG_HV2G1	Y4FN_RHISN	LRP1_CHICK	YHZ8_YEAST	ARAA_SALTY	MEFD_HUMAN	COMA_NEIGO	PULA_THEMA	HELY_MYCTU
-	Н	Н	Н	Н	٦	-1	Н	Н	Н	Н	Н	Н	Н	-1	-	-	Н	П	Н	Н	П
271	172	175	350	280	179	179	179	089	585	372	421	459	522	269	4543	321	200	521	691	843	906
11.2	11.1	10.7	10.7	10.6	9.4	9.3	9.3	7.0	6.8	6.7	6.7	6.7	6.7	6.7	6.7	9.9	9.9	9.9	9.9	9.9	9.9
156	155	149	150	148	131	130	130	86	95	93	94	93	94	94	94	85	92	92	92	92	93
24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	ن			(4)				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	Homo.				Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,	lams J.M., Cory S.;	promotes cell survival	•					I., Kawarabayasi Y.,	Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;	"Prediction of the coding sequences of unidentified human genes. VI	
	193 AA.		+	odal	1			Ve	e;				Berr	Ä	i1y,						G >	z	nic	:
	19		2		; : •			ta;	nid				-:	ы	fam						Ohti	jime	٥Ę٦	
	::		9	1.0	271)	•		nia	IOMi				D.C	iker	7						. :	iiya	es	1
	PRT;	_	, d	noti	AA0			CF	1; 1				ang	, B	PC.						71	<u>م</u>	Jenc	
	STANDARD;	/Dol 25 Grostod	(No.) 35 Last so	oi NOV-1997 (Rel. 35, Last apportation update)	APOPTOSIS REGULATOR BCL-W (KIAA0271),	LW.	Homo sapiens (Human).	etazoa; Chordata;	Eutheria; Primates; Catarrhini; Hominidae; Homo.		M N.A.	58615.	olmgreen S.P., Hua	, Sutherland G.R.,	vel member of the	Oncogene 13:665-675(1996).		M N.A.		MEDLINE; 97191544.	eki N., Ishikawa F	naka A., Kotani H.	of the coding sequ	THE OF THE PROPERTY.
	7	7	0	26	Ä	BC	ens	ž	Pr		FRO	963	Ĭ,	Ā.	ou	13:(FROI	AIN	971	Š,	Tai	e o	i
1	BCLW_HUMAN	Q92843; 01-NOV-19	NOV-19	NOV - 19	PTOSIS	BCL2L2 OR BCLW.	o sapi	aryota	heria;		SEQUENCE FROM N.A.	MEDLINE; 96358615.	son L.	kins N	1-w, a	odene		SEQUENCE FROM N.A.	TISSUE-BRAIN;	LINE;	ase T.	ra 0.,	edicti	athor odn
5	BCI	200	10	01-	APO	BCL	HOM	Euk	Eut	[1]	SEO	MED	Gib	Jen	"bc	Ouc	[2]	SEO	TIS	MED	Nag	Oha	"Pr	() E
RESULT	95	A F	1 5	i i	DE	N S	SO	8	ဗ	RN	RР	RX	RA	RA	RŢ	RL	RN	RP	Z S	КX	RA	RA	RŢ	E

-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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3; Gaps

34; Mismatches 32; Indels

76; Conservative

Matches

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especially by rescuing cells from apoptosis

The present sequence represents "Deprenyl" (RTM)-induced protein (DIP),
a novel protein in neural cells. This protein is induced by the
neuroactive drug "Deprenyl" (RTM). DIP 1 and compounds which modulate
its activity can be used for the diagnosis and treatment of neuro-
degenerative disorders, particularly apoptosis in neural cells. Such
apoptosis is associated with diseases such as Alzheimer's, Parkinson's
and Huntington's, as well as cerebellar degeneration and oligodendrocyte
Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6: Page 46: 75pp; English.

This protein sequence comprises human BCL-XL, a protein capable of blocking or suppressing NF-kapa B (NF-kB) activation. A claimed method of genetically modifying a mammalian endothelial cell to render it less susceptible to an inflammatory or other immunological stimulus comprises inscrining into the cell to expressing the cell such that NF-kB activation of the cell; DNA encoding an anti-apoptotic protein able to inhibit NF-kB, and inhibited in the presence of the the cellular activating stimulus. Suitable anti-apoptotic proteins include A20 (see W31528), BCL-2.

C see W31529), BCL-XL and A1 (see W31531) and their deletion mutants capable of inhibiting NF-kB, such as polypeptides comprising amino cacid residues 5-24, 86-100, 129-148 and 180-195 of BCL-XL. Also calmed are: (1) a mammalian endothelial cell modified by the above
                                                                                                                                                                                                                                                                                                                                                                      77 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 136
                                                                                                                                                                                                                                                                                                                                                                                                              41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 VFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160
                                                                                                                                                                                                                                                                             Score 623; DB 1; Length 225;
Pred. No. 1.06e-47;
34; Mismatches 32; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant endothelial cell containing DNA encoding anti-apoptotic protein - is less susceptible to inflammatory response and is useful for generating tissues or organs for transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human anti-apoptotic BCL-XL protein.
BCL-XL; anti-apoptotic protein; human; nuclear factor-kappa B;
NF kappa B; inhibitor; organ transplant; tissue transplant;
inflammation; gene therapy; endothelial cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mammal comprising DNA encoding an anti-apoptotic protein of a different species. The method can be used to generate donor endothelial cells or graftable tissues or organs for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          method: and (2) a non-human transgenic or somatic recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-A0C-1997.
13-FEB-1997; EC0676.
19-ARR-1996; US-634995.
14-FEB-1996; US-601515.
(NOWE) NOVARTIS AG.
Bach FH, Ferran C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transplantation into recipient species. Sequence 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 KGQERFNRWFLTGMTVAGVVLLGSL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W31530 standard; Protein; 233 AA.
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 52.4%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bach FH, Ferran (WPI; 97-424975/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
WO9730083-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W31530;
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Score 623; DB 1; Length 233; Pred. No. 1.06e-47;

Ouery Match Best Local Similarity 52.4%;

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Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases desearative diseases.

This sequence represents a novel protein, bcl-w, encoded by the mouse this sequence represents a novel protein, bcl-w, encoded by the mouse to bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischemaia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant bel-w for the approach.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Sequence 192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                    SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
                                                                                                                                                                                                                                                                                                                                         121 VQEWMYAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
                                                                                                                                                                                                                                                                                                                                                                                                                       1 HPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                       1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRFF 60
                                                                                                                                                                                                                                                                               2 PTPASTPDTRALVADEVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRTF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse bcl-w protein.
Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 7.82e-108;
0; Mismatches 0; Indels
                                                                                                                                                           Length 192;
                                                                                                                                                                                                    Indels
                                                                                                                                                             Score 1326; DB 1; I
Pred. No. 7.33e-117;
8; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams JM, Cory S, Gibson LM, Holmgreen SP; WPI; 97-489635/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              screening of potential modulators. Sequence 168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W36048 standard; Protein; 168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis; degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 Match
Local Similarity 100.0%;
hes 168; Conservative
                                                                                                                                                             78;
Local Similarity 94.3%;
Local Similarity 94.3%;
Les 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-1997; AU0199.
27-MAR-1996; AU-008965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ALVTVGAFFASK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 ALVTVGAFFASK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; T96578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp.
WO9735971-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1997
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                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W36048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                               62
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This is the amino acid sequence of the CDNA clone Bc1-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory alseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FSDLAAQLHVIPGSAQQRFIQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEDLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-1997.
21-DEC-1996; E05800.
12-JAN-1996; GB-000660.
12-JAN-1996; GB-000660.
Furst P, Tatton WG, Waldmeier P;
WPI; 97-384980/35.
New isolated "Deprenyl" (RTW)-induced protein - used to develop products for use in the diagnosis and treatment of neural disorders,
                                                                                                                                                         20-NOV-1998 (first entry)
Amino acid sequence of the CDNA clone Bcl-like (HAICH29).
Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
Bmmunological disorder; autoimmune disease; anti-infectious agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Deprenyl" (RTM)-induced protein 1.
Deprenyl-induced protein; neuroactive drug; neural cell; apoptosis; neurodegenerative disorder; oligodendrocyte; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotides and encoded polypeptides - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.1%; Score 1041; DB 1; Length 365; Best Local Similarity 96.5%; Pred. No. 1.22e-88; Matches 139; Conservative 5; Mismatches 0; Indels
121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA 168
                    121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA 168
                                                                                                                                                                                                                                                                                                                                                     (AUCK-) AUCKLAND UNISERVICES LTD.
(HUMA-) HUMAN GENOME SCI INC.
Feng P, Gentz RL, Krissansen GW, Ni J, Rosen CA,
Su JY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 12A-12D; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 QVQEWMVAYLETRLADWIHSSGGW 144
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                                                                                                                      W59884 standard; Protein; 365
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                                                                                                                                                                                                                                                                                            21-JAN-1998; U00960.
21-JAN-1997; US-034205.
21-JAN-1997; US-034204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     98-414099/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; V41925
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                                                                                                                                                                                                                                      Homo sapiens.
WO9831800-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
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                                                                                                                                        W59884;
                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                         The present associated with Boltwan protein associated with Boltwan by a final model to associated with Boltwan by a protein associated with Boltwan by a bisclosure; Page 37; 52pp; English.

The present sequence is described of a derivative of human Boltwan by a pro-survival member of the Boltz family that is widely expressed and which is essential for spermatogenesis.

The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine carries a mutation is at least one allele of the human or murine substantially infertile, but possess no other major abnormalities a determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or cherwise facilitating spermatogenesis in animals, or which can induce infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 QVQDWIVAYLETRLADWIHSSGGWADFTALXGDGALEDARRLREGNWA-VSTVVTGAVAL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                      N-PSDB, X25134. An animal model exhibiting reduced levels of a Bcl-w protein and/or \ensuremath{\mathsf{An}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T96577.

Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bcl-w; apoptósis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease.
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Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 96.0%; Score 1331; DB 1; L
Best Local Similarity 93.8%; Pred. No. 2.34e-117;
Matches 181; Conservative 9; Mismatches 2;
                                                                                                                                                                                                        16-SEP-1997; AU-009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Adams J, Cory S, Gibson L, Koentgen F, Print C;
WPI; 99-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMRA-) AMRAD OPERATIONS PTY LTD.
Adams JM, Cory S, Gibson LM, Holmgreen SP; WPI; 97-489635/45.
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27-MAR-1996; AU-008965.
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                                                                                                                                                                              16-SEP-1998; AU0764
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WO9735971-A1.
                                                                                                  WO9913710-A1.
                                                                            Homo sapiens
                                        animal model
                                                                                                                                          25-MAR-1999
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   NAMES OF THE PART 
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Novel bcl-y homologues of the rat and human bcl-2 protein - useful modulating programmed cell death.

Novel bcl-y homologues of the rat and human bcl-2 protein - useful claim 2; Columns 19-22; 26pp; English.

Claim 2; Columns 19-22; 26pp; English.

The present sequence represents a mammalian bcy-1 protein.

The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis).

Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzineimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infurction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis- conditions where cells under go premature cell death as a result of triggers which may or may not be apparent.

They may also be used in this way to develop cell lines which remain
This sequence represents a novel human protein, bcl-w, encoded by the bcl-2 gene family and extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat Mol-y protein; Robl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; multiple sclerosis; myocardial lifarction; vitally induced cell death; aging; spinal cord injury; amplicateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
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Pred. No. 2.34e-117;
9; Mismatches 2;
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Best Local Similarity 93.8%;
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                                                                                                                                                                                                                                                                                                                                                                    181; Conservative
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11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
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                                                                                                                                                                                                                                                                          193 AA;
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16-MAR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth e.g. cancers the standard of the bol-2 family, components the mammalian bol-y protein is a member of the bol-2 family, components in the cell death pathway. The bol-2 family have both apoptotic activity and the apoptosis blocking activity bol-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.
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                                                                                                                                                                                                                                                  61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human bcl-y protein.
bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
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Pred. No. 5.93e-118;
8; Mismatches 2; Indels
                                        Length 193;
                                                                                     Indels
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                                        Score 1337; DB 1; 1
Pred. No. 5.93e-118;
8; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W61392 standard; Protein; 193 AA.
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Best Local Similarity 94.3%;
Matches 182; Conservative
                                             96.5%;
94.3%;
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                                                                  Local Similarity 94.3%;
hes 182; Conservative
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23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
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WPI: 98-446079/38.
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193 AA;
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US5789201-A.
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  Sequence
                                             Query Match
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                                                                                          Matches
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Novel bol-y homologues of the rat and human bol-2 protein - useful for modulating programmed cell death bisclosure; Columns 19-20; 26pp; English.

Disclosure; Columns 19-20; 26pp; English.

The specification describes rat bol-y protein (Rbol-y) and human bol-y protein (Hbol-y). Rbol-y and Hbol-y are homologues of the bol-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbol-y and Hbol-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial confarction, vitally induced cell death, ading, spinal cord injuries and amyotrophic lateral sclerosis- conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune cell death in, and hence
                                                                                              Protein sequence of the specification.

Protein sequence of large sequence of injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 VQDMIVAYLETRLADMIHSSGGWADFTALXGDGALEDARRLREGNWA-VSTVVTGAVALG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCABSVNKEMEPLVGQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PIPASTPDTRALVADEVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
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Pred. No. 1.86e-117;
7; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 9
Y05532 standard; Protein; 193 AA.
Y05532,
05-JUL-1999 (first entry)
Human Bcl-w protein essential for spermatogenesis.
T 8
W97393 standard; Protein; 192 AA.
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Local Similarity 95.3%;
Les 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-NOV-1997; 978523.
23-FEB-1996; US-012201.
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Sequence 192 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99-214150/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
US5883229-A.
16-MAR-1999.
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04-AUG-1998.

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The mammalian bol-y protein is a member of the bol-2 family, components in the cell death pathway. The bol-2 family have both apoptotic activity and the apoptosis blocking activity. bol-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell
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Claim 2: Page 33: 52pp; English.

The present sequence is human Bcl.w, a pro-survival member of the present sequence is human Bcl.w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for Spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl.w gene (see X25132-35) or in a gene associated with bcl.w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FSDLAAQLHVTPGSAQORFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGGGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                              Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-1999 (first entry)
Human Bcl-w protein essential for spermatogenesis.
Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.9%; Score 1343; DB 1; Length 193; 95.3%; Pred. No. 1.50e-118; ative 7; Mismatches 1; Indels
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16-SEP-1998; AU0764.
16-SEP-1997; AU-009228.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Adms J, Cory S, Glbson L, Koentgen F, Print C; WPI; 99-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (05530 standard; Protein; 193 AA.
                                                                                                                                                                                                                          Example; Fig 3A; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 95.3%;
les 184; Conservative
                11-FEB-1997; 798897.
23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
(COCE-) COCENSYS INC.
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                                                                                                                                                                                                  growth e.g. cancers
                                                                                                                      98-446079/38.
                                                                                                                                         N-PSDB; V283333.
                                                                                                                                                                                                                                                                                                                                                                                        death is desired
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WO9913710-A1.
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                                                                                               Guastella J
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Matches
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Novel bol. 4 homologues of the rat and human bol-2 protein - useful for modulating programmed cell death

Claim 1. Columns 17-18, 26pp; English.

Claim 1. Columns 17-18, 26pp; English.

C The present sequence represents human bol-y protein (Hbol-y). The specification also describes rat bol-y protein (Rbol-y). Rbol-y and Hbol-y are homologues of the bol-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbol-y and Hbol-y and Hbol-y are homologues of the bol-2 protein thought to be involved in programmed cell death pathway. If they act as cell death in disruption of cell death pathway. If they act as cell death in disruption of Alzheimer's Disease, neural and muscular degenerative diseases

C Gespecially multiple sclerosis, myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral

C sclerosis conditions where cells under go premature cell death as a cesul to firingers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, collonged cell life span such as cancer (especially kaposi's sarcoma and collonged cell life span such as cancer (especially spansis's sarcoma and clusses cell death in, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The human belly protein.

The human belly protein.

Rat belly protein; Rbelly; human belly protein; Hbelly; bell-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
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                                                                                                                                                                                                     Indels 1; Gaps
                                                                                                                                                                                                                                               1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRT 60
other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including
                                                                                                                                                                                                                                                                                           1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                            genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.
                                                                                                                                                              Length 193;
                                                                                                                                                         Score 1341; DB 1; L
Pred. No. 2.38e-118;
8; Mismatches 1;
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W97392 standard; Protein; 193 AA.
                                                                                                                                                       Match 96.8%;
Local Similarity 94.8%;
les 183; Conservative
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23-FEB-1996; US-012201.
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                                                                                                               193 AA;
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US5883229-A.
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                                                                                                               Sequence
                                                                                                                                                         Query Match
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US5789201-A
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US5883229-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein associated with Bol-w, a pro-survival member of the Claim 2; Page 35; 52pp; English.

Claim 3; Page 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWAVSTVVTGAVALG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse Bcl-w protein essential for spermatogenesis.
Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.0%; Score 1345; DB 1; Length 193; 95.9%; Pred. No. 9.52e-119;
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Adams J, Cory S, Gibson L, Koentgen F, Print C;
WPI; 99-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
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W97391 standard; Protein; 193 AA.
                                                                                                                                                                                                                                                                                                                                               T 2
Y05531 standard; Protein; 193 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-1999 (first entry)
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16-SEP-1998; AU0764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 AA;
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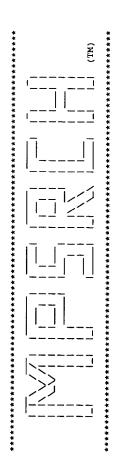
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Novel bcl-y homologues of the rat and human bcl-2 protein - useful PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful For modulating programmed cell death homologues (clumns 15-18; 26pp; English.

The present sequence represents rat bcl-y protein (Rbcl-y). The confication also describes human bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in conformance cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, consecially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral corditions where cells under go premature cell death as a consection of triggers which may or may not be apparent. They may also be consected in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, conditions way be used to treat conditions associated with the consection and auto/haperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
The rat bol-y protein.

The rat bol-y protein.

The rat bol-y protein.

Rat bol-y protein, Rbol-y; human bol-y protein; Hbol-y; bol-2 homologue; programmed cell death; apoptosis, necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease, neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aping; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autolmmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 QVQDWMYTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
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bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 193;
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02-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-FEB-1996; US-012201.
11-FEB-1997; US-798897.
25-NOV-1997; US-978523.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COCE-) COCENSYS INC.
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25-NOV-1997; 978523.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Jun 23 14:17:41 2000; MasPar time 7.56 Seconds 601.720 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-155-327B-9 (1-192) from US09155327B.pep 1386 Description: Perfect Score: Sequence:

1 MPTPASTPDTRALVADFVGY......VTGAVALGALVTVGAFFASK 192

Scoring table:

PAM 150 Gap 11

Post-processing:

188963 seqs, 23686106 residues

Searched:

Minimum Match 0% Listing first 45 summaries

a-geneseq36 1:geneseqp Database:

Mean 32.566; Variance 139.419; scale 0.234 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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NO	9-12	52e-1]	9-1]	9-11	9-17	-5	9-17	9-13	3-11	34e-11	9-13	3-10	22e-88	06e-47	9-47	9-47	9-47	14e-41	60e-40	60e-40	60e-40	9-40	60e-40
Pred.	8.04e-12	.52	.50e-	.50e-1	.38e-	.93e-	.93e-1	.86e-	.34e-1	.346	.33e-1	.82e-1	. 22	.06	.06e-4	.06e-4	.06e-4	.146	.60	.606	9.	3.60e-40	. 60
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ion	Bcl-w protein	Bcl-w protein	The rat bcl-y protein.	Rat bcl-y protein	Human Bcl-w protein	The human bcl-y protei	Human bcl-y protein	Protein sequence of	Human Bcl-w protein	Human bcl-w protein	Mammalian bcî-y protei	Mouse bcl-w protein	Amino acid sequence of		Human anti-apoptotic	Human thymus BCL-XL	Bcl-XL protein	A human Bcl-2 protein.	Bcl-2-alpha	bc1-2	bcl-2 protein	Soge	bc1-2.
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61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

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3.60e-40	3.60e-40	6.99e-40	6.99e-40	6.99e-40	6.99e-40	6.99e-40	3.29e-39	3.29e-39	3.29e-39	5.13e-39	7.98e-39	5.46e-35	5.46e-35	5.46e-35	5.46e-35	5.46e-35	5.46e-35	6.19e-32	4.84e-28	4.84e-28	8.75e-20
Sequence of bcl-2-alph	Human oncogene bcl-2 p	Apoptosis-blocking pro	Human Bcl-2 mutant pro	A murine Bcl-2 protein	Human Bcl-2 wild-type	Apoptosis-blocking pro	Chicken lymphoid BCL-X	Human Bcl-2 mutant pro	Apoptosis-blocking pro	Mouse BCL-x gamma.	Human BCL2.	Human thymus BCL-2.	Human anti-apoptotic B	A human Bcl-2-beta pro	Human bcl-2 beta prote	Human bcl-2 protein.	bcl-2 polypeptide.	Sequence of bcl-2-beta	Human Bcl-2 mutant pro	Apoptosis-blocking pro	Human thymus BCL-X1.
P80987	R47344	W01019	W94346	W87811	W94345	W01018	R68884	W94347	W01020	W48312	W02383	R68886	W31529	W87813	R71405	R70332	W96319	P80988	W94348	W01021	R68885
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239	239	232	232	236	239	239	190	232	232	235	239	202	202	202	202	202	202	202	229	229	63
39.3	39.3	39.1	39.1	39.1	39.1	39.1	38.6	38.6	38.6	38.5	38.3	35.4	35.4	35.4	35.4	35.4	35.4	33.1	30.2	30.2	23.8
545	545	542	542	542	542	542	532	535	535	533	531	491	491	491	491	491	491	459	418	418	330
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MYELOID CELL LEUKEMIA PROTEIN MCL-1 (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
                                                                                                                                                                                        58 DFHVESIDTARIIFNQVMEKEFEDGIINWGRIVTIFAFGGVL-LKKLPQEQIALDVGAYK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 -PNWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEWNVAYLETRLVDWIHSSGGWAEFTA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 PGRASSAVMEKALETLRRVGDGVMQKHELAFQGMLRKLEIKKEDDLQAVCEVAAQVFNDG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 VTNWGRVVTLISFGAFVAKHLKSINQEKCITSLAGIITDALVSSKREWLMSQGGWEGFVD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEE R.M., GILLET G., BURNSIDE J., THOMAS S.J., NEIMAN P.; "Role of Nr13 in regulation of programmed cell death in the bursa of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 AGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
11.2%; Score 156; DB 13; Length 211;
Best Local Similarity 22.0%; Pred. No. 8.69e-10;
Matches 29; Conservative 32; Mismatches 70; Indels 1; Gaps
                                                                                                                       Score 162; DB 11; Length 172;
Pred. No. 8.16e-11;
20; Mismatches 31; Indels 7; Gaps
HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SOFER L., BURNSIDE J.;
SUBMITTED (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF120210; AAD31644.1; -.
PROSITE; PS01080; BH1; 1.
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Last sequence update)
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       NAKAYAWA K., NAKAYAMA K.-I.;
Int. Immunol. 0:0-0(1998).
EMBL; U23780; AAB97956.1; JoineD.
MGD; MGI:1278335; BC12ald.
PROSITE; PS01080; BHJ; I.
PROMIP PF00452; BC1-2; 1.
SEQUENCE 172 AA; 20048 MW; 1B340DDD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 211 AA; 23143 MW; DEE4E997 CRC32;
                                                                                                                                                                                                                                                                                                    211 AA.
                                                                                                                                                                                                                         117 QVSSFVAEFIMNNTGEWIRRNGGWED 142
                                                                                                                                                                                                                                        | | | : :: :||| : :1121 QVQEWMVAYLETRLVDWIHSSGGWAE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fabricius.";
Genes Dev. 13:718-728(1999).
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                                                                                                                       Query Match 11.6%;
Best Local Similarity 32.6%;
Matches 28; Conservative
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                                                                                                                         BARTLING B., HOFFMANN J., HOLTZ J., SCHULZ R., HEUSCH G., DARMER D.; "EXPression of apoptosis-associated genes in hibernating and stunned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 DPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KUTAY U., IZAURRALDE E., HARTMANN E., GOERLICH D.; "A human homologue of yeast Mtrl0p and its role in nuclear protein
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0
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 119; DB 4; Length 923;
Pred. No. 8.14e-04;
15; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 144; DB 6; Length 80;
Pred. No. 8.91e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 GDDINRRYDSEFQAMLQHLQPTAENAYEYFTKIASSLFESGINWGRVV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myocardium of pig.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ001204; CAA04598.1; ...
HSSP: Q16611; 1BXL.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AJ133769; CAB42643.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
SEQUENCE 923 AA; 104203 MW; 1661174C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                     80 AA; 8818 MW; 973BE2D0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: Fri Jun 23 14:15:48 2000 Job time : 36 secs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               440 VLFIMAAIAKSVDPENNPTLVEVLE 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 FLFGAALCAESVNKEMEPLVGQVQE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.5%;
Best Local Similarity 32.9%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEAR TRANSPORT RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 35.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                 SEQUENCE FROM N.A.
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Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                      1 80
                                                                                                                                                                                                                                                                                                                                    Apoptosis.
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NON_TER
SEQUENCE
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Q9Y3R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9Y3R2;
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LT 12
055179
055179;
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"Up-regulated expression of murine Mcll/EAT, a bcl-2 related gene, in the early stage of differentiation of murine embryonal carcinoma cells and embryonic stem cells."
Biochim. Biophys. Acta 1398:335-341(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAO J.R., WANG J.M., LEE S.F., PENG H.W., LIN Y.H., CHOU C.H., CHOU J.C., HUANG H.M., CHOU C.K., KUO M.L., YEN J.J.Y., YANG-YEN H.F.; "mcl-1 is an immediate-early gene activated by the granulocyte-macrophage colony-stimulating factor (GM-CSF) signaling pathway and is one component of the GM-CSF vlability response."; Mol. Cell. Biol. 18:4883-4898(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GEAGAAGRRALETLRRVGDGVQRNHETAFQGMLRKLDIKNEGDVKSFSRVMVHVFKDGVT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 NWGRLVAFFLFGAALCAESVNK-EMEPLVGQVQEWWVAXLETRLVDWIHSSGGWAEFTAL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 NWGRIVTLISFGA-FVAKHLKSVNQESFIEPLAETITDVLVRTKRDWLVKQRGWDGFVEF 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
::|::: :|:| |:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: ||||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: |||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 167; DB 11; Length 331;
Pred. No. 1.11e-11;
30; Mismatches 64; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEO C.P., HSU S.Y., HSUEH A.J.W.; "Sequence of rat Mcl-1, a Bcl-2-related gene."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
                                                                                                                                                                                                                                    01-MAY-1997 (TrEMBLrel. 03, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
EAT/MCL-1 PROFEIN (MCL1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; Q07817; 1MAZ.
MGD; MGI:L01769; MG11.
PROSITE; PS01080; BH1; 1.
SEQUENCE 331 AA; 35217 MW; 3103C5FE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 AA
                                                                                                                                                                           331 AA
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                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Cell. Biol. 18:4883-4898(1
EMBL; U35623; AAC31790.1; -.
EMBL; AF063886; AAC27929.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match
Local Similarity 25.2%;
hes 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE OF 1-65 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 FHVQDLEGGIR 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=129/SVJ;
MEDLINE; 98336293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 98322120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Q9Z1P3
Q9Z1P3;
                                                                                                                                                                    P97287
P97287;
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1D 099
DA 001
DD 01
DD 01
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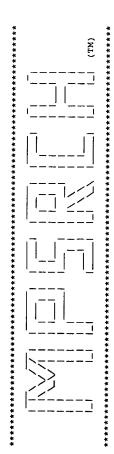
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 EIISRY-LREQATGSKDAKPLGEAGAAGRRALETLRRVGDGVQRNHETAFQGMLRKLDIK 218
                                                                                                                                                                                                                                                                                                                                            219 NEDDVKSFSRVMTHVFKDGVTNWGRIVTLISFGAFVAKHLKSINQESCIEPLAESITDVL 278
                                                                                                                                                                                                                                                                                                                                                                        6; Gaps
                                                                                                                                                                                                                                                                       16 DFVG-YKLRQKGYVC-GAGP-GE-GPAADPLHQAMRAAGDEFETRFRRFFSDLAAQLHVT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
B-CELL LEUKEMIA/LYMPHOMA 2 RELATED PROTEIN AID (A1-D PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 11 PRELIMINARY; PRT; 172 AA.
055177 (055177) (1758 (TEMBLTEL. 06, Created)
01-JUN-1998 (TEMBLTEL. 06, Last sequence update)
01-NUV-1999 (TEMBLTEL. 12, Last annotation update)
B-CELL LEUKEMIA/LYMPHOMA 2 RELATED PROTEIN AIB (A1-B PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Medazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-129/SV; TISSUE-LIVER;
HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,
HATAKEYAMA K., NAKAYAMA K.-I.;
Int. Immunol. 0:0-0(1998).
EMBL; U23778; AAB97954.1; -.
EMBL; U23777; AAB97954.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 163; DB 11; Length 172;
Pred. No. 5.48e-11;
                                                                                                                                  Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Mismatches 31; Indels
                                                                                                                                                                                       Indels
                                                                                                                            Score 165; DB 11; 1
Pred. No. 2.47e-11;
33; Mismatches 75;
EMBL, AF115380; AAD13295.1; -.
HSSP, Q07817; 1MAZ.
PROSITE; PS01080; BH1; 1.
SEQUENCE 330 AA, 35195 WW; CC87F2E0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20048 MW; FA16DF6C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 VRTKRDWLVKQRGWDGFVEFFHVQDLEGGIR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 ETRLVDWIHSSGGWAEFTALYGDGALEEARR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 QVSSFVAEFIINNTGEWIRRNGGWED 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 QVQEWMVAYLETRLVDWIHSSGGWAE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129/SV; TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.7%;
Best Local Similarity 32.6%;
Matches 28; Conservative
                                                                                                                                  Query Match 11.8%;
Best Local Similarity 24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1278326; BC12alb.
PROSITE; PS01080; BH1; 1.
PFAM; PF00452; BC1-2; 1.
SEQUENCE 172 AA; 20048
                                                                                                                                                                                       37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCL2A1D OR A1D
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MEDLINE; 98024143.
HSU S.Y., KAIPIA A., MCGEE E., LOMELI M., HSUEH A.J.W.;
"Bok is a pro-apoptotic Bol-2 protein with restricted expression in reproductive tissues and heterodimerizes with selective anti-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 GDELE-QIRPSVYRNVARQLHIPLQSEPVVTDAFLAVAGHIFSAGITWGKVVSLYSVAAG 133
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INCHARA N., EKHTERAE D., GARCIA I., CARRIO R., MERINO J., MERRY A., CHEN S., NUNEZ G.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF027954: AAB87418.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                           Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQDSFVDLY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HE X.J., JIN K.L., GRAHAM S.H., SIMON R.P.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR136230; AAD33683.1; -.
PROSITE; PS01259; BH9: 1.
PROSITE; PS01260; BH4_1; 1.
SEQUENCE 170 AA: 19031 MW; 8B29C9C1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat), and Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 LAVDCVRQAQPAMVHALVDCLGEFVRKTLATWLRRRGGWTD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | :: | |:: | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |
                                                                                                                                                                                                                                                                                                       Score 207; DB 11;
Pred. No. 6.91e-19;
11; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 175; DB 11;
Pred. No. 4.38e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23456 MW; 29761D17 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLEEL. 05, Created)
01-JAN-1998 (TrEMBLEEL. 05, Last sequ
01-NOV-1998 (TrEMBLEEL. 08, Last anno
BCL-2-RELATED OVARIAN KILLER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                    14.8%;
                                                                                                                                                                                                                                                                                                                                                       Similarity 58.3%;
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 12.5%;
Best Local Similarity 24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSU S.Y., HSUEH A.J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00452; Bcl-2;
SEQUENCE 213 AA; 23
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-MOUSE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR MTD.
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LT 6
035425
035425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9W6F2;
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ID 03
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TISSUE-OVARY, UTERUS;
HSU S.Y., HSUEH A.J.W.;
"A splicing variant of the Bcl-2 member Bok with a truncated BH3
domain induces apoptosis without dimerization with anti-apoptotic Bcl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSU S.Y., KAIPIA A., MCGEE E., LOMELI M., HSUEH A.J.;
"Bok is a pro-apoptotic Bcl-2 protein with restricted expression in
reproductive tissues and heterodimerizes with selective anti-apoptotic
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                 87 GRIMTIFTFGGLL-TKKLQEHGVQLTGEEKE-KISYFITEYI--INNKAAWIDANGGWEN 142
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 99190706.
LEE R.M., GILLET G., BURNSIDE J., THOMAS S.J., NEIMAN P.;
"Role of Nr13 in regulation of programmed cell death in the bursa of
                                                                                                                                                                                                                                                                                                                                   27 GPAQTRVAHVLRNIASSLQDQTEEALRPFLDRIDITSVDVAKRIFNGVMEEKFADGNTNW 86
                                                                                                                                                                                                                                                                                                                                                      36 GPAADPIHQAMRAAGDEFETRFRTFSDLAAQLHVTPGSAQQR-FTQVSDELF-QGGPNW 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 SPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASPAPGG-RLAEVCTVLLRLGITWG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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9
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 KVVSLYSVAAGLAVDCVRQAQPAMYHALVDCLGEFVRKTLATWLRRRGGWTD 131
                                                                                                                                                                                                                                                                   DB 13; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 170;
                                                                                                                                                                                SOFER L., BURNSIDE J.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF120211; AAD31645.1; -.
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 proteins.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF051093; AAC61928.1; -.
SEQUENCE 170 AA; 18729 MW; 79B4BBE6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
                                                                                                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                                                                 Pred. No. 3.32e-12;
46; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.97e-12;
                                                                                                                                                                                                                        174 AA; 20095 MW; 70F5FDAA CRC32;
                                                                                                                                                                                                                                                                 Score 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.1%; Score 169;
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01-NOV-1998 (TrEMBLrel. 08, Last sequ
01-NOV-1998 (TrEMBLrel. 08, Last anno
BCL-2-RELATED OVARLAN KILLER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 GFLTKFERRSPLSFSTITDIFAAVLSL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 GALEEARRIREGNWASVRTVLTGAVAL 180
                                                                                                                               Genes Dev. 13:718-728(1999).
                                                                                                                                                                                                                                                                 12.2%;
Similarity 20.4%;
30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 22.3%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bcl-2 family members.";
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TISSUE=OVARY, UTERUS;
MEDLINE; 98024143.
                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                  Fabricius."
                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                   Query Match
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088857
38°°
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229 AA; 25099 MW; E82B3DFB CRC32;
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                                                                                                                                                                                                                                                                    BCL2-LIKE (BCL-X-GAMMA).
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   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                      035843
035843;
035843;
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Q9WUI5
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                                                                                                                                                                                                                                                                                                                                                                                                                               145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-B66/CBA; TISSUE-THYMUS;
MEDLINE; 98051053.
YANG X.-F., WEBER G.F., CANTOR H.;
"A novel Bcl-x isoform connected to the T cell receptor regulates apoptosis in T cells.";
Immunity 7:629-639(1997).
EMBL; 051278; AAC53459.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                            Score 630; DB 11; Length 233;
Pred. No. 1.97e-106;
30; Mismatches 35; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-HOLSTEIN; TISSUE-THYMUS;
REYES R.A., COCKERELL G.L.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
BCL2-LIKE (BCL-XL).
                                                                                                                                                                                                                                                          MGD; MGI:88139; Bc121.
PROSITE; PS01080; BH1; 1.
PROSITE; PS010289; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4,1; 1.
PROSITE; PS01451; BC1-2; 1.
SEQUENCE 233 AA; 26033 MW; A4A14278 CRC32;
                                              233 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 KGKEGFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::|| | | ::|
161 RLREG-N-WASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSTIE; PS01060; BH1; 1.
PROSTIE; PS01258; BH2; 1.
PROSTIE; PS01259; BH3; 1.
PROSTIE; PS01260; BH4_1; 1.
PFAM; PF00452; BC1-2; 1.
NON_TER 229 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U92434; AAB53319.1; --
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Best Local Similarity 53.8%;
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                              PRELIMINARY;
      181 GALVTVGAFFASK 193
                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCL-2 (FRAGMENT)
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                                                                                                                                                                                                                                                                                                                                                                     78;
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002718
002718;
                                   LT 2
035844
035844;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 AAGPAPSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARERFATVVEELFRD 130
                                                                                                                                                                                                                             131 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDSIALWMTEYLNRHLHTWIQDNGGWDAFVE 190
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                              30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRFFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=B6/CBA; TISSUB-THYMUS;
MEDLINE; 9005103;
YANG X.-F., WEBER G.F., CANTOR H.;
"A novel Bcl-x isoform connected to the T cell receptor regulates apoptosis in T cells.";
minunity 7:629-639(1997).
EMBL; U51277; AAC53458.1; -.
HSSP; P53563; IAF3.
                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 18.3%; Score 535; DB 11; Length 235; Local Similarity 59.0%; Pred. No. 6.46e-86; les 62; Conservative 24; Mismatches 19; Indels
   Length 229;
Query Match 42.2%; Score 590; DB 6; Length 229
Best Local Similarity 44.5%; Pred. No. 9.22e-98;
Matches 73; Conservative 46; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 LFGAALCAESVNKEMEPLVGQVQEWNVAYLETRLVDWIHSSGGWA 145
                                                                                                                                                                                                                                                                                                                                                                                     150 LYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                   191 LYGP-SM---RPLFDFSWLSLKALLSLAL-VGACITLGAYLGHK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26122 MW; FB0B0207 CRC32;
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-NOV-1999 (TrEMBLrel. 12, Last ann
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STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:88139; Bc121.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
PFAM; PP00452; Bc1-2; 1.
SEQUENCE 235 AA; 26122 MW;
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Jun 23 14:15:12 2000; MasPar time 18.46 Seconds 724.726 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-155-327B-7 (1-193) from US09155327B.pep 1397 Description: Perfect Score:

1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193 Sequence:

PAM 150 Gap 11 Scoring table:

225878 seqs, 69334122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb112

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 5:sp_haye 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 44.702; Variance 83.297; scale 0.537 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	5.726-273	1.97e-106	9.22e-98	6.46e-86	6.91e-19	4.38e-13	3.32e-12	4.97e-12	1.11e-11	2.47e-11	5.48e-11	8.16e-11	8.69e-10	8.91e-08	8.14e-04	1.63e-03	1.72e-01	2.36e-01	2.36e-01	4.44e-01
Description	BCL-W.	BCL2-LIKE (BCL-XL).	BCL-2 (FRAGMENT).	BCL2-LIKE (BCL-X-GAMMA	BCL-X SHORT.	BCL-2-RELATED OVARIAN	PROTEIN A1.	BCL-2-RELATED OVARIAN	EAT/MCL-1 PROTEIN (MCL	MCL-1 PROTEIN.	B-CELL LEUKEMIA/LYMPHO	B-CELL LEUKEMIA/LYMPHO	MYELOID CELL LEUKEMIA	BAK PROTEIN (FRAGMENT)	NUCLEAR TRANSPORT RECE	B-CELL LEUKEMIA/LYMPHO	C42C1.4 PROTEIN.	HYPOTHETICAL 46.4 KD P	TRANSPORTIN-SR.	SIMILAR TO BCL-FAMILY
ΩI	966880	035844	002718	035843	Q9WUI5	035425	Q9W6F2	088857	P97287	Q9Z1P3	055177	055179	Q9W6F1	077738	Q9Y3R2	055178	044971	069657	Q9Y5L0	036423
DB	1	11	9	11	11	1	13	11	11	11	11	11	13	9	4	11	ស	~	4	14
% Query Match Length DB	193	233	229	235	170	213	174	170	331	330	172	172	211	80	923	128	1259	451	975	168
% Query Match	98.6	45.1	42.2	38.3	14.8	12.5	12.2	12.1	12.0	11.8	11.7	11.6	11.2	10.3	8.5	8.4	7.4	7.3	7.3	7.2
Score	1378	630	290	535	207	175	170	169	167	165	163	162	156	144	119	117	103	102	102	100
Result No.		7	3	₹	Z.	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	70

21 101 7.2 378 2 053318 HYPOTHETICAL 42.6 KD P 22 100 7.2 440 1 Q9YFI3 F4662.9 PROTHEIN. 24 100 7.2 451 5 P90814 F4662.9 PROTHEIN. 24 100 7.2 505 1 Q50517 HYPOTHETICAL 55.1 KD P 25 100 7.2 505 1 Q50517 HYPOTHETICAL 55.1 KD P 26 99 7.0 572 5 01865 D2013.5 PROTEIN. 29 98 7.0 572 5 019345 NHR-25 PROTEIN. 29 98 7.0 572 1 Q6505 SURRACE ENVELOPE PROTEIN. 30 66 8 75 14 Q5505 SURRACE ENVELOPE PROTE 31 95 6.8 148 14 P87523 SURRACE ENVELOPE PROTE 32 6.8 148 14 P87531 SURRACE ENVELOPE PROTE 34 95 <	3.24e-01 4.44e-01 4.44e-01 4.44e-01 6.07e-01 8.28e-01 2.07e+00 3.78e+00 2.07e+00 3.78e+00 3.78e+00 2.80e+00 2.80e+00	3.706.00
101 7.2 378 2 100 7.2 440 1 100 7.2 440 1 100 7.2 505 1 99 7.1 967 5 98 7.0 572 14 98 7.0 572 14 96 6.9 757 14 95 6.8 148 14 95 6.8 148 14 95 6.8 597 14 95 6.8 1053 2 95 6.8 630 7 95 6.8 630 2 95 6.8 630 2 97 6.7 130 14 94 6.7 279 14	HYPOTHE: TYPEIN. TYPEIN. TYPEIN. TYPEIN. THE TO THE TYPEIN. THE TY	HODOH
101 7.2 378 100 7.2 440 100 7.2 451 100 7.2 505 100 7.2 505 99 7.1 967 98 7.0 572 1 96 6.9 7.7 1 95 6.8 148 1 95 6.8 1053 1 97 6.7 131 1 94 6.7 585 1	053318 0997F13 0272814 0272814 0218965 0918965 0918965 0918965 0918965 097781 092784 092784 092784 092711 092711 092714 0057148 065604	2000
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1000 1000 1000 1000 1000 1000 1000 100	378 440 440 505 505 505 521 571 757 757 757 663 663 663 130 131 131 131 131 131 131 131 131 13	1
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ALIGNMENTS

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#title Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma.
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##cross-references GB:M16506; NID:9468335; PIDN:AAA37281.1; PID:9387110
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                                                                                                                                                             76 VATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 AAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELFRD 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137332 *type complete transforming protein (bcl-2-beta) - human forming protein (bcl-2-beta) - human formal_name Homo sapiens *common_name man 03-war-1993 *sequence_revision 03-war-1993 *text_change 23-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVMSB1 #type complete transforming profein Delta - mouse fransforming profein Delta *common_name house mouse #formal_name Mus musculus *common_name house mouse 31-Dec-1988 *sequence_revision 31-Dec-1988 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGPMWGRLVAFFLFGAALCAESVNKEMEPLVGQVQEMWVAYLETRLVDWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWWTEYLNRHLHTWIQDNGGW 192
                                                                                                                                                                                                                                                                                                       preliminary; nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #Superfamily bol transforming protein
alternative splicing; transforming protein
#length 199 #molecular-weight 22299 #checksum 7397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGW 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #length 206 #molecular-weight 22440 #checksum 5581
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Pred. No. 3.39e-76;
28; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 206;
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                                                                                                                                                                                                                                                                                                                                                              ##superfamily bcl transforming protein
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Best Local Similarity 49.6%;
Matches 58; Conservative
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##molecule_type DNA
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##residues 1-2
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Search completed: Fri Jun 23 14:14:23 2000 Job time: 20 secs.
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                                                                                                         ##residues 1.232 ##label CAZ
##cross-references EMBL:211961; NID:g62969; PIDN:CAA78018.1; PID:g62970
##cross-references EMBL:211961; NID:g62970
##cross-references EMBL:2122 #molecular-weight 25839 #checksum 1516
#title Molecular cloning and DNA sequence analysis of cDNA encoding
   chicken homologue of the Bcl-2 oncoprotein.
#cross-references MUID:92379084
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#Journal J. Immunol. (1994) 153:4388-4398
#title Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
#cross-references MUD:95052604
                                                                                                                                                                                                                                                                                                         79 GCAAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTATGRFVAVVEELFRDGVNWV 138
                                                                                                                                                                                                                                                                                                                                                                                   139 RIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGWDAFVELYGN- 197
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                                                                                                                                                                                                                                                                                                                                   36 GPAADP-LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGDNWG 94
                                                                                                                                                                                                                                                                        Gaps
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bcl-x transmembrane deleted - mouse
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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h-bcl-xbeta
#formal_name Homo sapiens #common_name man
21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change
16-Jul-1999
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#length 214 #molecular-weight 23900 #checksum 9730
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                                                                                                                                                                                                                                  DB 2; Length 232;
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                                                                                                                                                                                                                              Score 567; DB 2; Length 232
Pred. No. 5.16e-88;
38; Mismatches 41; Indels
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##residues 1-214 ##label RES
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                                                                           preliminary
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Best Local Similarity 46.5%;
Marches 74; Conservative
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                         Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler,
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Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #title bcl-x, a bcl-2-related gene that functions as a dominant
regulator of apoptotic cell death.
#cross-references MuID:93364977
#accession A47537
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#formal_name Gallus gallus #common_name chicken
03-May-1994 #sequence_revision 03-May-1994 #text_change
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                                                                Biochem. Biophys. Res. Commun. (1998) 248:147-152 Identification of a human cDNA encoding a novel bcl-x
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                                                                                                                                                                                                                                                                                                                                                             #molecular-weight 25290 #checksum 864
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                                                                                                                                                                                             ##residues 1-227 ##label BAN
##cross-references GB:U72398; NID:g1622940; PIDN:AAB17354.1;
PID:g1622941
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Pred. No. 6.90e-82;
20; Mismatches 24;
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#accession JE0203
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Best Local Similarity 53.7%;
Matches 65; Conservative
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Best Local Similarity 59.8%;
Matches 67; Conservative
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JE0203
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CLASSIFICATION #su
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Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology (1995) 136:232-241

Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
                                                                                                                                                                                                                                                                            ##residues 1-236 ##label RES ##scross-references GB:L14680; NID:9408946; PIDN:AAA53662.1; PID:9408947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #formal_name Rattus norvegicus #common_name Norway rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
16-Jul-1999
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                                                                                                     Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
Gene (1994) 140:291-292
Cloning and sequencing of a cDNA encoding the rat Bcl-2
#formal_name Rattus norvegicus #common_name Norway rat 29-May-1998 #sequence_revision 29-May-1998 #text_change
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#length 233 #molecular-weight 26122 #checksum 8310
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#length 236 #molecular-weight 26550 #checksum 8001
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PID:g1004377
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pred. No. 4.62e-90;
31; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
41.4%; Score 579; DB 2; Length 236
Best Local Similarity 44.6%; Pred. No. 1.80e-90;
Matches 74; Conservative 43; Mismatches 44; Indels
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#accession 167431
                                                                                                                                                                                           MUID: 94193015
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Best Local Similarity 50.3%;
Matches 73; Conservative
                                          16-Jul-1999
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BCL-X-Long -
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Cell (1987) 49:455-463
Molecular analysis of mbcl-2: structure and expression of the
murine gene homologous to the human gene involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
#journal Nucleic Acids Res. (1992) 20:4187-4192

#title Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1.236 ##label NEG ##cross-references GB:L31532; GB:M16506; NID:9468336; PIDN:AAA37282.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *superfamily bcl transforming protein alternative splicing; mitochondrion; transforming protein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 VATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWWTEYLNRHLHTWIQDNGGWDAF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87
                                                                                                                                                                                                                                                                            Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   $24390  #type complete transforming protein (Bcl-2) homolog - chicken #formal_name Gallus gallus #common_name chicken 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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                                                                                                                              TVMSA1 #type complete
transforming protein bcl-2-alpha - mouse
#formal_name Mus musculus #common_name house mouse
#formal_pame Mus musculus #common_name house
#1-nca-1988 #sequence_revision 31-Dec-1988 #text_change
18-Jun-1999
A25960; E37332
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Biochim. Biophys. Acta (1992) 1132:109-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary; nucleic acid sequence not shown; not compared with conceptual translation
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                         follicular lymphoma.
#cross-references MUID:87187643
#accession A25960
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Matches 74; Conservative
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cell (1986) 47:19-28
Cloning and structural analysis of cDNAs for bcl-2 and a
hybrid bcl-2/immunoglobulin transcript resulting from the t
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##residues 1-95,'A',97-109,'G',111-236,'S',238-239 ##label TSU
##cross-references GB:M13994; NID:g179366; PIDN:AAA51813.1; PID:g179367
##note this sequence has been corrected in reference A37332
                                                                                                                                                                                                        Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
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#title Analysis of the structure, transcripts, and protein products of bcl-2, the gene involved in human follicular lymphoma.
#cross_references_MUID:86259760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer, S.J.
#journal EMBO J. (1988) 7:123-131
#title Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2--Ig fusion gene in lymphoma.
#cross-references MUID:88196071
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##residues 1-58,'T',60-116,'R',118-239 ##label CLE
##cross-references GB:M14745; NID:9179370; PIDN:AAA35591.1; PID:9179371
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                                                                                transforming protein bcl-2, splice form alpha - human #formal_name Homo sapiens #common_name man 31-bcc-1988 #sequence_revision 07-Jun-1996 #text_change 18-Jun-1996
                                                                                                                                                                                                                                                                                                                                                                      nucleic acid sequence not shown; not compared with
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this report is a correction
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#accession A24420
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blocks apoptosis in hematopoietic cells
*superfamily bcl transforming protein
alternative splicing; B-cell lymphoma; follicular lymphoma;
proto-oncogene; transforming protein; transmembrane protein
*length 239 #molecular-weight 26266 #checksum 8323
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#journal Endocrinology (1995) 136:232-241
#title Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong #cross-references WUID:95129487
#accession 167432
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BCL-2 - rat (fragment)
BCL-2 - rat (fragment)
#formal_name Rattus norvegicus #common_name Norway rat
26.Jul-1996 #sequence_revision 26-Jul-1996 #text_change
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PID:g1004379
FICATION #superfamily bol transforming protein
#length 236 #checksum 9134
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Best Local Similarity 45.1%; Pred. No. 6.59e-92;
Matches 74; Conservative 44; Mismatches 41;
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Pred. No. 2.72e-91;
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##molecule_type | 1-236 ##label RES
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Best Local Similarity 45.2%;
Matches 75; Conservative
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#journal J. Immunol. (1994) 153:4388-4398
#title Clohing and molecular characterization of mouse bcl-x in and T lymphocytes.
#cross-references WUID:95052604
                            85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
41 PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bcl-x long - mouse
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                         S51761 #type complete
BCL-X protein - rat
#formal_name Rattus norvegicus #common_name Norway rat
07-May-1995_#sequence_revision 01-Sep-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #superfamily bcl transforming protein
#length 233 #molecular-weight 26130 #checksum 6378
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PID:g607177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues
##cross-references EMBL:X82537; NID:g607176; PIDN:CAA57887.1;
                                                                                                                                                                                                                                                                                                                                                                                                                           Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994
$51762
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submitted to the EMBL Data Library, November 1994
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Pred. No. 7.19e-98;
30; Mismatches 36; Indels
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                                                                                                               1-233 ##label MIC
                                                                                             205 KGQERFNRWFLTGMTVAGVVLLGSL 229
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Best Local Similarity 53.18;
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#journal Nucleic Acids Res. (1992) 20:4187-4192
#title Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
#cross-references MUID:92375724
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mitochondrion; transforming protein; transmembrane protein
#length 233 #molecular-weight 25687 #checksum 99
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                                                                                                                                                                                                                                                                                                                        #checksum 5739
                                                                                                                                                                                                                                                     ##cross_references EMBL:X83574; NID:9695622; PIDN:CAA58557.1;
PID:9695623
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                                ##cross-references EMBL:U10101; NID:g506647; PIDN:AAA82173.1;
PID:g506648
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44.0%; Score 615; DB 2; Length 233
Best Local Similarity 53.1%; Pred. No. 7.19e-98;
Matches 77; Conservative 30; Mismatches 36; Indels
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#length 233 #molecular-weight 26132
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                                                                                                                                                                                                          ##Slacus
##molecule_type mRNA
"""......Anoa 1-233 ##label KAM
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Best Local Similarity 46.6%;
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##molecule_type mRNA
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Jun 23 14:14:03 2000; MasPar time 12.24 Seconds 743.766 Million cell updates/sec Run on:

Tabular output not generated.

Description: Perfect Score:

>US-09-155-327B-7 (1-193) from US09155327B.pep 1397 1 MATPASAPDTRALVADFVGY......LTGAVALGALVTVGAFFASK 193 Sequence:

PAM 150 Gap 11 Scoring table:

142080 segs, 47172406 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

Mean 45.096; Variance 88.441; scale 0.510 1:pirl 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	4.47e-98	7.19e-98	7.19e-98	4.11e-92	6.59e-92	2.72e-91	1.80e-90	4.62e-90	4.89e-89	5.16e-88	4.13e-83	4.32e-82	6.90e-82	1,33e-76	3.39e-76	3.59e-74	3.59e-74	9.58e-55	7.46e-23	1.37e-21	1.37e-21	3.14e-21	4.75e-21
Description	apoptosis requlator b	BCL-X protein - rat	om	transforming protein		BCL-2 - rat (fragment	gene bcl-2 protein -	BCL-X-Long - rat	transforming protein	transforming protein	bcl-x transmembrane d	apoptosis requlator b	apoptosis requlator b	transforming protein	transforming protein		transforming protein	gene bcl-2 protein -	bcl-2-associated prot	bcl-2-associated prot	bcl-2-associated prot	Bak protein - human	bcl-2-associated prot
QI QI	B47537	S51761	149056	A37332	TVHUA1	I67432	I53744	167431	TVMSA1	S24390	149057	JE0203	A47537	D37332	TVMSB1	TVHUB1	B37332	I58194	D47538	138921	A47538	S58873	153295
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% Query Match Length DB	233	233	233	233	239	236	236	233	236	232	214	227	190	206	199	202	216	154	192	143	192	211	133
Query Match	44.1	44.0	44.0	42.0	41.9	41.7	41.4	41.3	40.9	40.6	38.9	38.5	38.4	36.6	36.4	35.7	35.7	28.8	16.8	16.3	16.3	16.2	16.1
Score	919	615	615	587	586	583	579	577	572	267	543	538	537	511	509	499	499	402	235	228	228	226	225
Result No.	1	7	e	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

24 225 16.1 211 2 558875 cdn-2 protein - human 25 218 15.6 218 15.6 218 2 B47538 bcl-2-associated prot 26 205 14.7 170 2 1649055 bcl-x short - mouse 27 201 14.4 176 2 167435 gene bcl-xshort protein 149 11.7 2 16773 gene bcl-xshort protein 150 10.7 177 2 16949 hemopoietic-specific 150 10.7 175 2 139055 Bcl-2 related - human 31 150 10.7 175 2 139055 Bcl-2 related - human 32 148 10.6 280 2 A53189 apoptosis suppressor 7.3 451 2 B70792 hypothetical protein 34 100 7.2 378 2 F70947 hypothetical protein 172 173 173 100 7.2 168 2 F70947 hypothetical protein 172 173 173 173 173 173 173 173 173 173 173	4.75e-21 1.68e-17 1.68e-17 1.68e-17 1.06e-13 4.20e-08 6.05e-08 5.05e-08 3.13e-01 5.69e-01 5.69e-01 5.69e-01 2.44e+00	4.31e+00 4.31e+00 3.25e+00 3.25e+00
225 16.1 211 2 208 14.7 170 2 209 14.7 170 2 183 13.1 177 2 155 11.1 172 2 150 10.7 350 2 100 7.2 280 2 101 7.2 378 2 100 7.2 440 2 100 7.2 440 2 100 7.2 440 2 100 7.2 460 2 95 6.8 630 2 95 6.8 668 2 97 6.7 250 2 98 6.7 250 2 98 6.7 250 2 98 6.7 250 2	cdn-2 protein - human bcl-2-associated prot bcl-x short - mouse gene bcl-xshort prote NR-13 protein - quail hemopoletic-specific Bcl-2 related - human BCL2 homolog MCL1 - h apoptosis suppressor hypothetical protein probable alkaline proconserved protein Flp ABC transporter sill?	hypothetical protein conserved hypothetica gag polyprotein . hum molybdopterin oxidore alpha-2-macroglobulin
225 218 205 205 14.7 203 14.7 183 13.1 149 10.7 100 7.2 100 7.2 100 7.2 100 7.2 100 7.2 100 7.2 100 7.2 100 7.2 100 7.3 95 6.8 95 6.8 95 6.7 94 6.7 94 6.7	\$58875 847538 164955 164435 164435 139055 44744 139055 44776 44779 47792 1703168 1703168 1703168 1703168 1703174 172784 172784 172784 172784 172784 172784	T08908- H69002 FOLJGG H69271 A53102
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APPLICATION NUMBER:

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Job time : 12 secs.
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Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: NOCKEMEYER, Stanley J.
TITLE OF INVENTION: BC1-x/Bc1-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE: 19930622
                                                                                    APPLICATION 19930622
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646008thrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD090
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
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TENCE 233 AA; 26063 MW; 275311 CN;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy
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US-08-661-479-59
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85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 44.1%; Score 616; DB 2; Length 233; Best Local Similarity 53.1%; Pred. No. 6.27e-44; Matches 77; Conservative 30; Mismatches 36; Indels
FILLING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARRATERISTICS:
LENGTH: 233 amino acids
                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECCLE TYPE: peptide
JENCE 233 AA; 26049 MW; 275801 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: Fri Jun 23 14:16:17 2000
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ADDRESSEE: Townsend and Townsend Khourie and Crew
                 Palo Alto
: California
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                                             94301
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US-08-081-448-6
                          STATE: Ca
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      TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MARKESON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
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Patent No. 5622852
GENERAL INFORMATION:
BEDLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: BC1.x/Bc1-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
                                                                                                                                                                                                                                                                                                                                                      Score 616; DB 3; Length 233;
Pred. No. 6.27e-44;
30; Mismatches 36; Indels
                                                                                             COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 AA
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CE 233 AA; 26049 MW; 275801 CN;
                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 2364
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 494-0792
TELEX: 706141
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 annino acids
TYPE: annino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 59, Application US/08333565
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APPLICANT: BARR, PHILIP J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.1%;
Matches 77; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                               FILING DATE:
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85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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Patent NO. 5646008
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                              ATORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
JENCE 233 AA; 26049 MW; 275801 CN;
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379 Lytton Avenue
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TYPE: amino acid
STRANDEDNESS: single
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Local Similarity 53.1%;
les 77; Conservative
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COMPUTER READABLE FORM:
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Sequence 7, Application US/08470670A Patent No. 5834309 Patent No. 5834309 5710045
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Local Similarity 53.1%;
Les 77; Conservative
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                                                                                                    CITY: Houston
STATE: Texas
                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                         2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Score 616; DB 4; Length 233;
Pred. No. 6.27e-44;
30; Mismatches 36; Indels
                                                                                              Vertebrate Apoptosis Gene:
Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 AA.
   233 AA.
                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
CURRENT APPLICATION DATA:
                                                                                           TITLE OF INVENTION: Vertebrate Apoptos
TITLE OF INVENTION: Compositions and NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                            TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 233 AA; 26049 MW; 275801 CN;
                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US94/07089 FILING DATE: CONCURRENTLY FILED
                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/081.448
FILING DATE: 22 JUNE 1993
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD090
TELECHOMONE: 512-320-700
TELEPHONE: 512-320-700
   PRT;
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                                                                    Sequence 7, Application PC/TUS9407089 GENERAL INFORMATION:
                                                   Sequence 7, Application PC/TUS9407089
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Best Local Similarity 53.1%;
Matches 77; Conservative
                                                                                                                                                                                                                                           CLASSIFICATION:
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US-08-470-670A-7
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   PCT-US94-07089-7
                                                                                      APPLICANT:
                                                                                                                                                         STATE:
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Pred. No. 6.27e-44;
30; Mismatches 36; Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,670A
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B. B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 AA.
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REGISPRATION NUBBR: 37,642
REFERENCE/DOCKET NUMBER: ARCD:090--1
TELECOMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,448
FILING DATE: 22-UTN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America ZIP: 77210
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SEQUENCE 233 AA; 26063 MW; 275311 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08471057
Patent No. 6015687
GENERAL INFORMATION:
APPLICANT: RIEFER, MICHAEL C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08471057
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SEQUENCE
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          121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
                                             1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 192;
                                                                                                                                                                                                     Sequence 5, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCES: 53
CORRESPONDENCES: STERRE, KESSLER, GOLDSTEIN & FOX P.L.L.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798 897
FILING DATE: February 11, 1997
CLASSIFCATION: 435
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Pred. No. 1.95e-112;
4; Mismatches 1;
                                                                                                                              192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION UNMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 192 AA; 20689 MW; 183185 CN;
                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                    Sequence 5, Application US/08798897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 192 amino acids
                                                                                                                               STANDARD:
                                                                                                                                                                                                                                                                                                                            ZIP: 20005
COMPUTER READABLE FORM:
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tes 187; Conservative
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                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION
TITLE OF INVENTION: Interaction of Proteins Involved in
TITLE OF INVENTION: a Cell Death Pathway
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 616; DB 4; Length 233;
Pred. No. 6.27e-44;
30; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Imbra, Richard J.
REGISTRATION NUMBER: 37,643
REFERENCE/DOCKET NUMBER: FP-LJ 1361
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: PCT/US95/04600
12-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application PC/TUS9504600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 AA; 26063 MW; 275311 CN;
                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application PC/TUS9504600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 KGQERFNRWFLTGMTVAGVVLLGSL 229
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 24
                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
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Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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California
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                                                                                        181 ALVTVGAFFASK 192
                                                                                                                                    182 ALVTVGAFFASK 193
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РСТ-US95-04600-24
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COUNTRY:
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CITY: Sa
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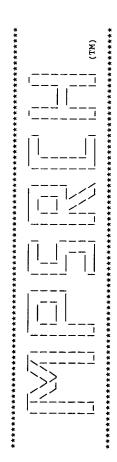
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                                121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
                                                                              1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
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1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF
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Pred. No. 1.58e-112;
                                                                                                                                                                                                                                                       APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATINE SYSTEM: PC-DOS/MS-DOS
SOFFWANDER: Patentin Release #1.0, Version #1.30
                                                                                                                                                          192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
JENCE 192 AA; 20701 MW; 181510 CN;
                                                                                                                                                          PRT;
                                                                                                                                                                                                                              Sequence 6, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
                                                                                                                                                                                                              Sequence 6, Application US/08798897
                                                                                                                                                                                                                                                                                                                                                                                                                                                      32,893
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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION UNMBER: 32,8
REFERENCE/DOCKET NUMBER:
                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.98;
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MEDIUM TYPE: Floppy
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121 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
                                                                                                      1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
                          0; Gaps
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Pred. No. 1.95e-112;
4; Mismatches 1; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: CEDEBURY 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ESEMOND, ROBER: 32,893
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 15540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICAMT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF SEQUENCES: 53
CORRESPONDENCE 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                  192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
JENCE 192 AA; 20689 MW; 183185 CN;
                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08978523
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STRANDEDNESS: not relevant
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                                                                                                                                                                                                                                                                                                       STANDARD;
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Best Local Similarity 97.4%;
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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STATE: DC
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                                                                                                                                                                                                                                                                                  JT 7
US-08-978-523-5
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61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFLFGAALCAESVNKEMEPLVG 120
                                                                                                         61 FSDLAAQLHVTPGSAQORFTQVSDELFQGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                             121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 192;
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: herewith
CLASSIFICATION: 424
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Pred. No. 1.58e-112;
1; Mismatches 2;
                                                                                                                                                                                                             192 AA.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
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192 AA; 20701 MW; 181510 CN;
                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
                                                                                                                                                                                                                                                                             Sequence 6, Application US/08978523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32,893
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 192 amino acids
amino acid
                                                                                                                                                                                                             STANDARD;
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Best Local Similarity
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                                                          Gaps
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                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICART: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                         193 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
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FILING DATE: herewith
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,89
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORREY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LE TYPE: protein
193 AA; 20820 MW; 185063 CN;
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                                                                                                                                                                                                                                                                            Sequence 3, Application US/08978523
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
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TYPE: amino acid
                                                                                                                                                                                                         STANDARD;
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Conservative
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Matches 188; Conserv
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                                                                                                                                                                                                                                   Gaps
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TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
   Length 193;
Score 1379; DB 1; Length 19:
Pred. No. 1.54e-113;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
PRIOR APPLICATION: 424
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ESPONG ROBERT WAS ATTORNEY/AGENT WAS ATTORNEY WAS ATTORNEY/AGENT WAS ATTORNEY/AGENT WAS ATTORNEY/AGENT WAS
                                                                                                                                                                                                                                                                                                                                                                                                193 AA.
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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 193 AA; 20832 MW; 183365 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
   Query Match 98.7%;
Best Local Similarity 98.4%;
Matches 190; Conservative
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STATE: DC
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                                    Gaps
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 Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.
                                    Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
 Score 1379; DB 2; I
Pred. No. 1.54e-113;
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                                    1; Mismatches
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MOLECULE TYPE: protein
JENCE 193 AA; 20820 MW; 185063 CN;
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Patent No. 5789201
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ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECHOMINICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08798897
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
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ilarity 97.4%;
Conservative
Query Match 98.7%;
Best Local Similarity 98.4%;
Matches 190; Conservative
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Best Local Similarity
Matches 188; Conser
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STATE:
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Jun 23 14:16:05 2000; MasPar time 5.04 Seconds 552.912 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-155-327B-7 (1-193) from US09155327B.pep 1397 Description: Perfect Score:

1 MATPASAPDTRALVADFVGY..........LTGAVALGALVTVGAFFASK 193

Sequence:

Scoring table:

PAM 150 Gap 11

145341 seqs, 14437480 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1 Database:

Mean 30.708; Variance 142.172; scale 0.216 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	1.54e-113	1.54e-113	1.90e-113	1.90e-113	1.58e-112	1.58e-112	1.95e-112	1.95e-112	6.27e-44	2.51e-41	2.51e-41	3.09e-41	3.09e-41	3.09e-41	3.09e-41								
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	Description	Seguence	Sequence	٠.			Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Sequence 1	Sequence 1									
	ΩI	US-08-798-	US-08-978-	us-08-798-	us-08-978-	US-08-978-	-864-80-SD	US-08-978-	us-08-798-	PCT-US95-0	PCT-US94-0	US-08-470-	US-08-471-	US-08-333-	US-08-081-	US-08-661-	US-08-471-	us-08-607-	us-08-607-	PCT-US95-0	US-08-337-	ns-08-826-	US-08-248-	us-08-82e-
	DB	7	7	Н	~	~	7	~	Н	4	4	7	٣	-	Н	7	Н	—	Н	4	~	~	Н	7
	Query Match Length	193	193	193	193	192	192	192	192	233	233	233	233	233	233	233	233	233	233	233	239	239	239	239
æ	Query	98.7	98.7	98.6	98.6	97.9	97.9	97.9	97.9	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	42.0	42.0	41.9	41.9	41.9	41.9
	Score	1379	1379	1378	1378	1368	1368	1367	1367	616	616	616	616	616	616	616	616	616	587	587	586	286	586	286
	Result No.	1	7	m	4	2	ø	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Mortis,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:693460
                                                                                                                                                                                                                   accccaggctcagcccagcaacgcttcacccaggtttccgacgaacttttccaagggggc 270
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                                                                                                                               151 gacgagtttgagacccgtttccgccgcaccttctctgacctggccgctcagctacacgtg 210
                                                                                                                                                    231 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 172
                                       gotgggcctggggaaggcccagccgccgccgctgcaccaagccatgcgggctgctgga 150
                                                                                                                                                                                                                                                               351 ACGCCCTTCACCGCGCGCGCGCCTTTGCCACGTGGTGGAGGAGCTCTTCAGGGACGGG 292
                                                                                   470 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTA-CCCTCCGCCAGGCCGGC 412
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1; Gaps
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA939725 515 bp mRNA EST 01-MAY-199 vz92all.rl Soares_thymus_2NbWT Mus musculus cDNA clone IMAGE:1344668 5' similar to gb:L31532_rnal Mouse bcl-2 gene encoding mbcl-2-beta (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
On Jan 19, 1998 this sequence version replaced gi:2285479.
Contact: Marna M/Mouse EST Project
WashID-HHMI Mouse EST Project
Washington University School of MedicineP
Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 gagacacgtctggctgactggatccacagcagtggcggctggg 433
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/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
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The WashU-HHMI Mouse EST Project
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/clone="IMAGE:1344668"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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Conservative
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Matches
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                                            91
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KEYWORDS
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                                                                                                                                                                                             Score 106.6; DB 40; Length 515;
Pred. No. 4.6e-17;
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60.6%;
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Best Local Similarity 60.6
Matches 175; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              Fax: 301 443 1706
Fax: 301 443 1706
Fax: 301 443 9890
Email: mESTefmail.nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
10.11sold track not found, Not I site shown in beginning of sequence
11s likely internal to the message. CDNA Library Preparation: M.B.
Soares Lab Clone distribution: NIH BMAP CDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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TAG_LIB-NIH_BMAP_M_S3.1
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                       On Jul 7, 1999 this sequence version replaced gi:5866278. Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
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                                                                                     Genome Res. 6 (9), 791-806 (1996)
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TAG_SEQ-TCAAG"
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T 3/1; double-stranded CDNA was ligated to ECO RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M-Fatima Bonaldo."
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cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tg92c06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116234 3' similar to gb:M13995 PROTEIN BCL-2-BETA (HUMAN);contains TAR1.t2
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I bases 1 to 471)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Onpublished (1997)

On Apr 7, 1998 his sequence version replaced gi:3035272.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov

Figurals programment and Alizada.
281 gccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagtgtcaacaaag 340
                                                                                                                                                                           341 aaatggagcctttggtgggacaagtccaggattggatcgtggcctacctggagacacgtc 400
                                                                                                                                                                                                        151 GTCGCATCGTGGCCTTTTTCTCCTTTGGCGGGGCACTGTGCGTGGAAAGCGTAGACAAGG 92
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/clone_lib="NoT_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MER22 repetitive element ;, mRNA sequence.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence stop: 445.
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UI-M-BH2.1-apn-b-04-0-UI.31 NIH_BMAP_M_S3.1 Mus musculus cDNA clone UI-M-BH2.1-apn-b-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Site_2: Not!, sex=Female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(df) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press" 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 ggagacgagtttgagacccgtttccgccgcaccttctctgacctggccgctcagctacac 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 gtgaccccaggctcagcccagcaacgcttcacccaggtttccgacgaacttttccaaggg 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AGCGTAGACAAGGAGATGCAGGTATTGGTGAGTNGGATCGCAGCTTAGATGGCCACTTAC 240
                                                                                                                                                                                      Email: genexpress@genethon.fr
Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: y3c-25b06
Insert Length: 1145 Std Error: 0.00
Seq primer: (-21)M13_universal
High quality sequence stop: 339.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                       Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
             Sep 21, 1992 this sequence version replaced g1:276079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="normalized infant brain cDNA" /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 ctggagacacgtctggctgactggatccacagcagtggcggctggg 433
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/clone="c-25b06"
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Best Local Similarity 62.2%;
Matches 178; Conservative
                                                                 Genexpress-Genethon
                                      Contact: Genethon
                                                                                                                                             Tel: 33169472800
                                                                                                                                                                Fax: 33160778698
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UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-Y0) was constructed as follows: PCR amplified cDRA inserts from previous library clones from which 3' ESTS had been derived were used as a driver in a hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (BODA) and SOBALES.
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I (bases 1 to 299)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Sebastiani-Kabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome and its expression

C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323 AACTGGGGTACCGGAGAGTTCAGTGATCTAACATCCCAGGTTCATATAACCCCAGGGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cagoccagoaacgottcacccaggtttccgacgaacttttccaagggggccctaactggg 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gccgtcttgtggcattctttgtctttggggctgccctgtgtgctgagagtgtcaacaaag 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 gggaaggcccagccgccgacccgctgcaccaagccatgcgggctgctggagacgagtttg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 agacccgtttccgccgcaccttctctgacctggccgctcagctacacgtgaccccaggct 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 CAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTTCGGGATGGGGTAAACTGGG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 GGGAGGTAATCCCCCATGGCAGCAGTGAAGCCAAGCGCTGAGAGGCTGGCGATGAGTTTG 324
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Pred. No. 1.6e-19;
0; Mismatches 133;
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TAG_TISSUE=Eye
TAG_SEQ=CATTG"
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ilarity 59.6%;
Conservative (
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Score 118.2; DB 7
Pred. No. 5.8e-20;
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/db_xref="taxon:10116"
/clone="UI-R-Y0-acg-g-07-0-UI"
/clone_lib="UI-R-Y0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
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                   20.3%;
62.3%;
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                                          Best Local Similarity 62.3
Matches 180; Conservative
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AI716839/c
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Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: poustka@mping-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKEZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            German Genome Project.

No s1 sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
                                                                                                   61 GCGGGGATTCAGTGACCTGACATCCCAGCTCCACATCACCACCCAGGGACAGCATATCAGA 120
                                                                                                                                                          233 getteacceaggtttecgaegaettttecaagggggeeetaaetggggeegtettgtgg 292
                                                                                                                                                                                                   121 GCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGG 180
                                                                                                                                                                                                                                                                                                                                                 241 TGGTGAGTCGGATCGCAGCTTGGATGCCCACTTACCTGAATGACCACCTTGG 300
113 ccgccgacccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttcc 172
                                                                              173 gccgcaccttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaac 232
                                                                                                                                                                                                                                             293 cattetttgtetttggggetgeeetgtgtgtgetgagagtgteaacaaagaaatggageett 352
                                                                                                                                                                                                                                                                                                                            353 tggtgggacaagtccaggattggatcgtggcctacctggagacacgtctggctgac-tgg 411
                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL134785 584 bp mRNA EST 29-DEC-1999 DKFZp547K2090_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547K2090 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                    1 CCACNGGAGCAGTAAAGCAAGCGCTGAGGGAGGCAGGCGACGACTTTGAACTGCGGTACC
                                                                                                                                                                                                                                                                       /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
145 c 173 g 116 t 6 others
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On Jul 7, 1999 this sequence version replaced g1:5866255.
Contact: Poustka A.J.
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Max-Planck Institute for Molecular Genetics
Innestrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131128
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/clone_lib="547 (synonym: hfbr1)"
/tissue_type="brain"
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/db_xref="taxon:9606"
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/lab_host="X1-2blue"
                                                                                                                                                                                                                                                                                                                                                                                                            412 atccacagcagtggcggctggg 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                301 ATCCAGGAGAACGCCGGCTGGG 322
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Email: msoares@blue.weeg.ulowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
POLYA-NO.
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/lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)"
/note="vector: pT7T3D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI.R-YO
library is a subtracted library derived from an Individually-tagged normalized whole-eye (minus the lens)
library. The driver for the subtraction consisted of a
pool of all previous libraries (UI-R-AO, UI-R-AI, UI-R-EO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 404)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 ccgacgaacttttccaagggggccctaactggggccgtcttgtggcattctttgtctttg 307
                                                                                                                                      128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
                                                                                                                                                                                                        293 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 352
                                                                                                                                                                                                                                                                                 188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtcc 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCANGTATTGGTGAGTCCNGATC 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UI-R-Y0-acg-g-07-0-UI.s1 UI-R-Y0 Rattus norvegicus CDNA clone
UI-R-Y0-acg-g-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 Eckstein Medical Research Building Iowa City, IA 52242, Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On May 18, 1998 this sequence version replaced gi:3136946.
                                                                 ö
DB 79; Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                 0; Mismatches 109;
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High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3687

Fax: (206) 616-3687

Email: jwallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu). Clonefa may be purchased from http://www.htsc.washington.edu
PITCH: (info@fresgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 638 row: M column: 4
Seg primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 455)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                       AQ401160 455 bp DNA GSS 13-MAR-1999
HS_5062_A2_G02_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=638 Col=4 Row=M, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                        432 ggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgcggga 491
                                                                                                          261 GGGGGAGTTCACAGCTCTATACGGGGACGGAGCCTGGAGGAGGCGCGGGCGTCTGCGGGA 320
                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
  DB 109; Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.3%; Score 124; DB 106; Length 455; 88.7%; Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="Plate=638 Col-4 Row=M"
/clone_lib="RPCI-11 Human Male BAC Library"
                                              Indels
                                         . 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC, Hood L
Score 135.6; DB 10
Pred. No. 2.4e-24;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                High quality sequence stop: 455.
Location/Qualifiers
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      23.3%;
94.0%;
         Query Match 23.3%
Best Local Similarity 94.0%
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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COMMENT
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KEYWORDS
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Indels

17;

0; Mismatches

Matches 133; Conservative

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Best Local Similarity

432 ggcggacttcacagctctatacggggacgggccctggaggacgcacggcgtctgcggga 491

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/clone="IMAGES19817"
/clone="IMAGES19817"
/clone_lib="Soares_fetal_lung_NDHL19W"
/clone_lib="Soares_fetal_lung_NDHL19W"
/dev_stage="19 weeks"
/lab_bost="blubl0B (ampicillin resistant)"
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
/note="Organ: lung; Vector: pT7T3D (Pharmacia) primer
[5/-TGTACCAATCTGAGTGGGGGGGGGGGGGGGTGT] primer
[5/-TGTACCAATCTGAGTGGGGGGGGGGGGGGGTT]
/couble-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatina Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NDHH19W."
                                                                                                                                                                                                                                                                                                                                                                              za73d06.rl Soares_fetal_lung_NbHL19W Homo sapiens CDNA clone
IMAGE:298187 5' similar to SW:BCLX_HUMAN Q07817 APOPTOSIS REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson wustl.edu
This clone is available royalty-free through LLNL; contact the TMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: mob. REGARET
High quality sequence stop: 383.
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Pred. No. 1.7e-20;
0; Mismatches 119; Indels . 1; Gaps
                                                                             gggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactgggggccctggt 551
284 GGGGAACTGGGCATCAGTGAGAGACAGTGCTGACNGTGGCCGTGGCACTTGGGGCCCTTGT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 437)
Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                           18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785898.
Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .437
/organism="Homo sapiens"
                                                                                                                                                                                                           552 aactgtaggggccttttttgctagcaagtg 581
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   BCL-X.;, mRNA sequence.
W01420
W01420.1 GI:1273428
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62.78;
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Best Local Similarity 62.7%
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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CDNA synthesis with oligo dT Xba I (Xba I cloning site). RNA: stage 50-56 tadpoles, total brain tissue, GTC extraction method."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         library availability, please contact Pieter de Jong (Pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
Venter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                        296 totttgtetttggggetgeeetgtgtgetgagagtgteaacaaagaaatggageetttgg 355
                                                                                                                                                                                                                                                                                                                                                                             tgggacaagtccaggattggatcgtggcctacctggagacacgtctggctgactggatcc 415
                                                                                                                                                                                                                                                                                                                                                                                                                    65 IGCCACGGATTCAAGACTGGATGGTGACATATCTGGAGACAAACCTGAGAGGCTGGATTC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acagcagtggcggctgggcggacttcacagctctatacggggacggggccctggaggacg 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 cacggogtctgcggggaaggcaactgggcatgagtgagcacagtggtgacgggggccgtgg 535
                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: bbe@tigr.org Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 628)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 CCAGGAGCCAACGTGAGGGGAATTGGGCATCACTGAAGACTGTCTTAACTGGAGCGGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 AGAGCAATGGATGCTGGAATGGATTTCTAACTCTATAGGGGATGGTGCCATAGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
On Feb 19, 1999 this sequence version replaced gi:4145213.
On Feb 19, 1999 this sequence version replaced gi:4145213.
Chter_GSS: RPCI-11-352LS.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                     25.8%; Score 150; DB 71; Length 416; 70.3%; Pred. No. 5.2e-28;
                                                                                                                                                                                                                              85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 t
                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                  Best Local Similarity 70.39
Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: BAC ends.
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                                                                     BASE COUNT
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AQ532175
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                                                                                          ORIGIN
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1. .628 /organism="Homo sapiens" /db_xref="GDB:7635052" /db_xref="taxon:9606" /clone="RPCI-11-35215"

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bass 1 to 549)
Mahairas,G.C., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: jwallacegu, washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu, Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
Plate: 916 row: B column: 11
Seq primer: 77
Class: BAC ends
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI;
RPCIll Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                    432 ggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgcggga 491
                                                                                                                                                                                                                                                                                                                                                        233 GGCGGAGTICACAGCTCTATACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ665088 549 bp DNA GSS 23-JUN-1999 HS_5340_B1_A06_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=916 Col=11 Row=B, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                        DB 108; Length 628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="Plate=916 Col=11 Row=B"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                              23.9%; Score 138.8; DB 108; Length
95.3%; Pred. No. 3.9e-25;
Live 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                552 aactgtaggggccttttttgctagcaagtg 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353 AACTGTAGGGGCCTTTTTTGCTAGCAAGTG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 549.
                                                                                                                         237 g
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                                                                                                                         130 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                 Matches 143; Conservative
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Best Local Similarity
                                                                                                                           128 a
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AW048567/c DEFINITION

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REFERENCE AUTHORS

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JOURNAL MEDLINE COMMENT

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1 (bases 1 to 416)
Schutz, K., de la Bastide, M., Huang, E.N., Nascimento, L., Preston, R.,
Shah, R., Swaby, I., Shekher, M., Spiegel, L., Vil, M.D. and
McComble, W.R.
used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.

TAG_LIB=NIH_BMAP_M_S2
TAG_TGSUE=corpus-striatum
a 131 c 85 g 110 t
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za50h02.xl Xenopus EST library Xenopus laevis cDNA clone za50h02
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/note="Vector: Lambda Zap I; Site_1: XbaI; This library
was supplied by Holly Cline (Cold Spring Harbor Labs).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 gacgaactttccaaggggccctaactggggccgtcttgtggcatctttgtctttggg 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           431 GACGAACTITICCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTTGGG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed sequence tags from Xenopus Unpublished (1999) On Jun 5, 1998 this sequence version replaced gi:3189433. Contact: W. Richard McCombie
                                                                                                                                                                                                                                                                                                                                                                                                                64; Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Pari 516 367 8884
Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Xenopus EST library"
/tissue_type="total brain tissue"
/cell_line="W22-TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: za50 row: h column: 02
Seq primer: M13 universal forward primer
High quality sequence stop: 416.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        Score 179.2; DB 6-
Pred. No. 2.4e-35;
0; Mismatches 3
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/db_xref="taxon:8355"
/clone="za50h02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW159063.1 GI:6271092
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.8%;
Best Local Similarity 98.4%;
Matches 181; Conservative
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The sequence contained an oligo-dr track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized corpus striatum library cDNA library Preparation: M.B. Soares Lab Clone distribution: NH BMAP CDNA clones will be made available by the means that is soon to be determined. When NIH ecord will be updated accordingly when that means is determined. Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Clone="UI-M-BH1-alx-e-10-0-UI"
/clone_lib="NIH BMAP_M_S2"
/dev_stage="27-32 days"
/dev_stage="27-32 days"
/lab.host="DH108 (Life Technologies)"
/lab.host="Public (Pharmacia) with a modified
/lab.host="Stage (Pharmacia) with a modified
/lab.host="Stage (Pharmacia) with a modified
/lab.host="DH108 (Life Technologies)"
/lab.host="DH108 (Life Technologies)"
/lab.host="DH108 (Pharmacia) with a modified
/lab.host="DH108 (Life Technologies)"
/lab.host=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 431)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW048567 431 bp mRNA EST 18-SEP-1999 UI-M-BHI-alx-e-10-0-UI.sl NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-alx-e-10-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                            181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
                                                                                                                                                                                                                                      61 aggctgaggcagaagggttatgtctgtggagctggggcctggggaaggcccagccgccgac 120
                                                                                                                                                                                                cogotgoaccaagccatgoggotgotggagacgagtttgagacccgtttccgccgcacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                   334 TTCTCCGATCTGGCAGCTCAGCTGCATGTGACCCCGGGCTCGGCCCAGCAACGCTTCACC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                              Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Feb 18, 1999 this sequence version replaced gi:4297581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996)
97044477
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source

FEATURES

27-JAN-2000

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EST discovery in cattle Unpublished (2000)
Unpublished (2000)
Un Dec 20, 1995 this sequence version replaced gi:1133576.
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Weat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4360
Smail: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Design and use of four pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                                                                                           gcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctc 185
                                                                                                                                                                                                                149 GCACCAAGCCATGCGTGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adreas and andometrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (basés 1 to 433)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and
                                                                                                                                                                                      246 ttccgacgaacttttccaagggggcctaactggggccgtcttgtggcattctttgtctt
                                                                                                                                                                                                                                                                                                                                                                                                                                             AW326901 433 bp mRNA EST
20104 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTACAGGACG
Plate: 10 row: G column: 24
Seq primer: ATTTAGGGTGACACTATAG.
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/lab_host="DH10B"
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Library constructed by Bob Barstead. The C2C12 cell line (avallable from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins.
                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Bases 1 to 362)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                              AAS96919 362 bp mRNA EST 19-SEP-1997 vo21f08.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNa clone IMAGE:1050567 5' similar to TR:E123735 E123735 Rl MRNA.;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaggcagaagggttatgtctgtggagctgggcctggggaaggcccagccgccgccgct 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 gaccccagcctcaaccccagacacacgcgctctagtggctgactttgtaggctataggct 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1966)
On Dec 18, 1996 this sequence version replaced g1:1734345.
Contact: Marna M/Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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Pred. No. 3e-71;
0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
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/clone="IMAGE:1050567"
                                                                                                                                                                                                                              AA596919.1 GI:2412354
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  531 AGTGGGGGCT 540
                                                                                                                                                                                                                                                                                                      Mus musculus
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0; Gaps
  DB 80; Length 433;
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us-09-155-327b-8.rst

321.8 55.4 362 35 AAS96919 228.8 39.4 433 80 AM326901 710.0 20.0 421 64 AM326901	A CORPUBLIC CONTRACTOR	3	Contact: Mar Washington D
73 000	AA596919 VO21f08.r AW326901 20104 MAR	. 4 E1	4444 Forest Tel: 314 286
25.8 416 71	AW048567 UI-M-BH1- AW159063 za50h02.x	E E	Fax: 314 286 Email: mouse
23.9 628 108 23.3 549 109	AQ532175 RPCI-11-3 AQ665088 HS 5340 R	E1 F	his clone
21.3 455 106	AQ401160 HS_5062_A		GI:1009678
20.3 584 79	AL134785 DKFZp547K	. II	ed primer: High quality
20.0	AI716839 UI-R-YO-a F08773 HSC25B061 n	FEATURES	LOC
19.0 454 69	AW124015 UI-M-BH2.	***************************************	 Vor
19.0 471	AI401297 tg92c06.x		/st
17.9 472 43	AASSS/23 V2SZALL:I AT180733 ub91d09 r		
16.6 471 34	AA509753 vh52c06.r		200
12.1 1696 83	AF149300 Rattus no		8,
516	AW4189U3 DAIDGUD.X		? <
8.0 616 44	AI323048 mi41h10.y		
7.6 278 60	AV138827 AV138827		Ü
7.6 478 61	AI837675 UI-M-AKO-		Wa
7.6 497 27	AA016399 mg88g02.r		4.
7 6 500 07	ALSZOYLY MJSYDOL.X		119
616 26	M97433 mf95f12.rl		and Yeb
7.4 640 40	AA981864 ua36¤07.r) Pe
7.3 547 41	AT020744 ub01h12.r		DG G
7.3 418	AA458294 vq48c03.r		2.5
7.3 747 74	AW226585 up09f12.x		Ins
7.2 925 82	AL053013 Drosophil		sec
7.2 534 44	AI322704 mj39b01.y		
7.2 545 26	W42014 mb16g04.rl	BASE COUNT	98 a
7.1	ALUS3013 Drosophil AA049970 mi39b01 r	ORIGIN	
8 7.0 1201 83	AL106545 Drosophil		
6 7.0 714 64	AW072826 xa42e07.x	Query Match	
0 6.9 274 20	T29044 EST66242 Hu	Best Local Similarity	Simi
0 6.9 377 80	AW355100 37259 MAR	Matches 42	420; Conserv
	A1323521 MO5/DU2.X		
4 0.0 0.0 49			
2 6.6 844 82	ALOSAÇO DIOSOPHII	Db 112 ATG	ATGGGGACCCCAGC
6.4 521	AI599840 EST251543		
		Qy 61 agg	aggetgaggeagaa
SHINGHINGLIK			
OTHERNOTES		7	15000000000000000000000000000000000000
		Qy 121 ccg	ccgctgcaccaag
		Db 232 CCG	CCGCTGCACCAAG
AW258810 540 bp mRNA	EST 23-DEC-1999	 - 	
um74a02.yl Sugano mouse kidney mkia Mus	musculus cDNA clone	Oy 181 ttc	ttetetgacetgge
IMAGE: 2300906 5' SIMILAR to SW: BCLW_MOU	SE P/0345 APOPTOSIS		
AW258810	una sequence:	767	101640016
AW258810.1 GI:6631791		Qy 241 cag	caggtttccgacga
EST.			
house mouse.		DD 352 CAG	GTTTCCGAC
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia	Vertebrata; Mammalia;	y 301 qtc	gtctttggggctgc
Sutheria; Rodentia; Sciurognathi; Murid	ae; Murinae; Mus.	•	
(bases 1 to 540)	H 0,1000 C 1000 H	Db 412 GTC	GTCTATGGGGCTGC
darra, M., Hillier, L., Kucaba, T., Martin	,J., Beck,C., Wylle,T.,	136	***************************************
<pre>underwood, n., steptoe, m., Inelsing, b., Allen, m., bowers, i., Person, B., Swaller, I., Gibbons, M., Pape, D., Harvev, N., Schurk, R.,</pre>	Allen,m., bowers,r., ,D., Harvev,N., Schurk,R.,	VY 301 Caag	caagiccaggaris
itter, E., Kohn, S., Shin, T., Jackson, Y.	, Cardenas, M., McCann, R.,	Db 472 CAA	rGCAT
Waterston, R. and Wilson, R.			
The Washu-NCI Mouse EST Project 1999		Δ <u>γ</u> 421 agr	agragogace 430

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/note-*Organ: Kidney; Vector: pME18S-FL3; Site_1: DraIII (CACGYGTGS); Site_2: DraIII (CACCAYGTGS); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACGTGTGG, 3' site CACCATGTG). KnoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTGTGCTCTAAAAGCTGCG and 3' end primer CGACCTGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                         seest@watson.wustl.edu
is available royalty-free through LLNL ; contact the
ortium (info@lmage.llnl.gov) for further information.
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                                                                         USA
1998 this sequence version replaced gi:3137956.
arra M/WashU-NCI Mouse EST Project 1999
University School of Medicine
                                                                       t Park Parkway, Box 8501, St. Louis, MO 63108,
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86 1810
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                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:10090"
clone="IMAGE:2300906"
clone_lib="Sugano mouse kidney mkia"
                                                                                                                                                                                                                                                                                                          . .540
organism="Mus musculus"
strain="C57BL"
                                                                                                                                                                                                                                       : custom primer used
ty sequence stop: 465.
ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dev_stage="adult"
lab_host="DH10B"
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Query
Result
                                         July 4, 2000, 01:06:08; Search time 795.04 Seconds (without alignments) 2962.018 Million cell updates/sec
                                                                               1 atgccgaccccagcctcaac......gccttttttgctagcaagtg 581
                                                                                                                         9714632
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                             4857316 seqs, 2026611650 residues
                               OM nucleic - nucleic search, using sw model
                                                                                                                                                              summaries
                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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581
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Listing first 45
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em_est11:
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Perfect score:
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em_gss4:*
gb_gss5:*
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9b_est40:*

9b_est41:*

9b_est41:*

9b_est41:*

em_est31:*

em_est32:*

em_est32:*

em_est32:*

em_est33:*

em_est33:*

em_est43:*

em_est44:*

em_est
gb_est26:*
gb_est27:*
gb_est29:*
gb_est30:*
gb_est31:*
gb_est31:*
em_est20:*
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em_est24:*
em_est25:*
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gb_est34:*
gb_est35:*
gb_est36:*
gb_est37:*
gb_est37:*
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em_est29:*
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em_gss3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 2, Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Wicketrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93
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                                                                                                                                                                                                                          Sequence 4, Application PC/TUS9305651
GENERAL INFORMATION:
    TITLE OF INVENTION: A Gene Which Prevents Programmed Cell Death
    NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
    MEDIUM TYPE: diskette
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: PCT/US93/05651
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.5%; Score 125; DB 6; Length 5086; 58.9%; Pred. No. 3.7e-26; tive 0; Mismatches 150; Indels (
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; OTHER INFORMATION: /product= "Bcl-2"
PCT-US93-05651-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA to mRNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 5086 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.5
Best Local Similarity 58.9
Matches 215; Conservative
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PCT-US93-06251-2
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PCT-US93-05651-4
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Pred. No. 3.7e-26;
0; Mismatches 150; Indels
                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
CLASSIFICATION:
NAME: Didigilo, Frank S.
REGISTRATION NUMBER: 31,346
              ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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58.9%;
                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 5086 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 58.99
Matches 215; Conservative
                                                                                                           ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS:
                                                                                               USA
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Search completed: July 4, 2000, 01:24:30 Job time: 14818 sec

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Query Match
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Pred. No. 3.7e-26;
0; Mismatches 150; Indels
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTATION UNDRER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEFRAN: (415) 324-0880
TELEFRAN: (415) 324-0800
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5086 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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58.9%;
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Matches 215; Conservative
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LOCATION: 1459..2178
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HYPOTHETICAL: NO
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                                           NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 150; Indels
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
                                                                                                                                                 STREET: 1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY AGENT INFORMATION:
NAME: POTECT: NAME: DECENT
                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,600
REGISTRATION NUMBER: 33,600
RELECOMMUNICATION INFORMATION:
TELEPAN: (408) 436-2070
TELEPAN: (408) 436-2075
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 5086 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                       KX: U.S.A.
22202
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                                                                                                                                                                                                    STATE: Virginia
                                                                                                                                                                         Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                              ADDRESSEE:
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US-09-080-285-19
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Batent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bc1-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   0; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                21.5%; Score 125; DB 7; 58.9%; Pred. No. 3.7e-26;
            APPLICATION NUMBER: US/08/228,704
FILING DATE: 18-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 994,941
FILING DATE: 23-DEC-1992
APPLICATION NUMBER: 663,010
FILING DATE: 19-MAR-1991
APPLICATION NUMBER: 883,687
FILING DATE: 09-JUL-1986
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APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
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CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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CLASSIFICATION:
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US-08-465-485A-19
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US-08-365-486A-14
Sequence 14, Application US/08365486A
Fatent No. 584306
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 21.5%; Score 125; DB 3; Length 50
Best Local Similarity 58.9%; Pred. No. 3.7e-26;
Matches 215; Conservative 0; Mismatches 150; Indels
                                                                                                FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: FOLICHEW D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEFAN: (408) 436-2075
INFORMATION FOR SEQ ID NO: 19:
APPLICATION NUMBER: US 08/124,256 FILING DATE: 20-SEP-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/840,716 FILING DATE: 21-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 5086 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-465-485A-19
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Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Real
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                                                                              21.5%; Score 125; DB 3; Length 71
58.9%; Pred. No. 1.8e-26;
ative 0; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Arington STATE: Virginia COUTRY: Virginia COUTRY: U.S.A. COUTRY: U.S.A. ZOP: 2202 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/080,285
TELECOMMUNICATION INFORMATION:
         TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                         LENGTH: 717 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                               Query Match 21.59
Best Local Similarity 58.99
Matches 215; Conservative
                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: 1..717
US-08-465-485A-20
                                                                                                                        linear
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                                                                                                                        TOPOLOGY:
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Pred. No. 1.8e-26;
0; Mismatches 150; Indels
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* APPLICANT: Tsujimoto, Yoshide;Croce, Carlo A.

* TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE

*;SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                 3335-070-55 CONT
                                                                 PRIOR APPLICATION DATA:
APPLICATION UNDER:
TLING DATE: 20-SEP-1993
PRIOR APPLICATION UNDER: US 07/840,716
APPLICATION UNDER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION.

NAME: FORTNEY, Andrew D.

REGISTRATION NUMBER: 34,600

REFERENCE/POCKET NUMBER: 34,600

TELEPHONE: (408) 436-2075

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 717 base pairs

TYPE: nucleic acid

TYPE: nucleic acid

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.5%;
Best Local Similarity 58.9%;
Matches 215; Conservative (
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US-09-080-285-20
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5459251-1
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Gaps

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128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgccgcacttctctg 187
                                                                                                                                                        acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
                                                                                                                                                                                                   248 ccgacgaacttttccaaggggccctaactggggccgtcttgtggcattcttgtctttg 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Compositions and Methods TITLE OF INVENTION: Compositions and Methods NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee STRET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07089
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STRANDEDNESS: single
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21P: 77210
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LOCATION:
PCT-US94-07089-6
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Length 926;
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ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Sulte 400
                                         Indels
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Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INFURFION:
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
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 Score 134.6; DB 6;
Pred. No. 4e-29;
0; Mismatches 169;
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APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/465,485A FILLING DATE: 05-JUN-1995 CLASSIFICATION: 514
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 23.2%;
58.3%;
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                                         Matches 236; Conservative
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MEDIUM TYPE: Floppy
Ouery Match
Best Local Similarity
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CLASSIFICATION:
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United States of America
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Patent No. 5834309
Patent No. 5834309 5710045
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TELEFAX: (512) 474-7577
INFORMATION FOR SEG ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UN
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, LOCATION:
US-08-470-670A-6
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US-08-470-670A-6
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421 agtggcggctgggcggacttcacagctctatacgggggacggggccctggaggacgcacgg 480
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                                                                       cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacgggggccgtggcactg
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Pred. No. 4e-29;
0; Mismatches 169; Indels 0
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STREET: 321 No. 5646008th Clark Street, Suite 800
CITY: Chicago
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,448
FILING DATE: 19930622
                                                                                                                                           APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: No. 5646008thrup, Thomas E.
REGISTRATION NUMBER: 33,268
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
TELEFAX: 312-755-4489
                                                                                                                                                                                                                                                                 Sequence 5, Application US/08081448 Patent No. 5646008
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SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.2%;
Best Local Similarity 58.3%;
Matches 236; Conservative (
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; LOCATION: 135..836
US-08-081-448-5
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                                                                                                                                    574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,670A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thompson, Craig B. B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: ARCD:090--1 TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,448
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
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GENERAL INFORMATION
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
                                                                                                                                                                                                                                                                                                                            Score 497.4; DB 2;
Pred. No. 3e-131;
0; Mismatches 51;
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                                                                                                                                    1483.0140001
                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: ESEMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                            85.6%;
91.2%;
                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                          Query Match 85.6
Best Local Similarity 91.2
Matches 528; Conservative
                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: CDNA
US-08-798-897-2
                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                         TOPOLOGY: both
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US-08-978-523-2; Sequence 2, Application US/08978523; Patent No. 5883229

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                                                                        ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington
                                                                                                                                  COUNTRY.

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
GORTWARE: PatentIn Release #1.0, Version #1.30
           TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2 TITLE OF INVENTION: Homologue
                                                                                                                                                                                                                                                                           Guastella, John
                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid STRANDEDNESS: both
                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: CDNA
US-08-978-523-2
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| Patent No. 588329
| GENERAL INFORMATION:
| APPLICANT: Guastella, John
| TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
| TITLE OF INVENTION: Homologue
| NUMBER OF SEQUENCES: 53
| CORRESPONDENCE ADDRESS:
| ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
| STREET: 1100 New York Avenue, N.W., Suite 600
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-371-2540
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                                                                                                            Length 579;
                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.
                                                                                                              Score 540.6; DB 3;
Pred. No. 2.1e-143;
0; Mismatches 24;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                    LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                            Query Match 93.0
Best Local Similarity 95.9
Matches 555; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                    CDNA
                                                      TOPOLOGY: both
MOLECULE TYPE: CD
US-08-978-523-1
                                 TYPE: nucleic
STRANDEDNESS:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-978-523-1
US-08-978-523-2
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Listing first 45 summaries
                                                      OM nucleic - nucleic search, using sw model
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Query
Match Length DB
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28 29 30 30 31 31 31 31 31 31 31 31 31 31 31 31 31	Sequence 7, Appli Sequence 8, Appli Sequence 90, Appli Sequence 20, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 9, Appli Sequence 6, Appli Sequence 6, Appli Sequence 17, Appli Sequence 17, Appli Sequence 6, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli		Length 579; Indels 0; Gaps 0; gactttgtaggctat 60	ACTITGIAGGCIAI 60
20	57 57 59 84.4.4.4.7.6 54.4.4.7.6 54.6.4.6.7.0 524 524 524 524 524 524 524 524	ESULT 1 \$-08-798 897-1 \$-08-798 897	TOPOLOGY: both MOLECULE TYPE: CDNA S-08-798-897-1 Query Match Best Local Similarity 95.9%; Score 540.6; DB 2; Matches 555; Conservative 0; Mismatches 24; I atgccgaccocagcctcaaccccagcacacacgcctctagtggct	Db 1 AIGGCGACCCCAGCTCAACCCCAGACACGGGCTCTAGTGGCTGTG

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/db_xref="SPTREMBL:077737"
/translation="MSQSNRELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESE
AETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPWAAVKQALREAGDEFELRYR
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VLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLTGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (13-JAN-1998) Bartling B., Institute of Pathophysiology, Martin Luther University, Magdeburger Strasse 18, 06097 Halle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="transmembrane domain: 680-736; Bcl-2 homolgy domains: BH4: 56-115, BH3: 298-343, BH1: 428-487, BH2: 581-628"
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                                 341 aaatggagcetttggtgggacaagtecaggattggategtggeetaeetggagacaegte 400
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                                                                       485 AGATGCAGGTATTGGTGAGTCGGATCGCAACTTGGATGGCCACTTACCTGAATGACCACC 544
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Bartling,B., Hoffmann,J., Holtz,J., Schulz,R., Heusch,G. and
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/db_xref="G1:3288632"
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/db_xref="taxon:9823"
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Bartling, B.
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                                    281 gccgtcttgtggcattctttgtctttggggctgcctgtgtgctgagagtgtcaacaaag 340
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                                                                                                                                                                                                                                                                      401 tggctgactggatccacagcagtggcggctgggcggacttcacagctctatacggggacg 460
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336 AACTGAGGTACCGGAGGGCATTCAGTGACCTGACGTCCCAGCTCCACATCACCCCAGGGA 395
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Job time: 16645 sec
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Lee, T.L. and Canty, J.M. Direct Submission
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AF216205.1 GI:6959766
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Boise-L.H., Gonzalez-Garcia, M., Postema, C.E., Ding, L., Lindsten, T.,
Turka, L.A., Mao, X., Nunez, G. and Thompson, C.B.
bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death
Cell 74 (4), 597-608 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSQSNRELVVDFLSYKLSQKGYSWSQFSDVEBNRTEAPEGTESE
METSAINGNBSWHLADSPAWGATHSSLDAREVIPMAANYGALREADEPELRYR
METSAILGATAGOSFBQVNNELFRDGVNWGRIVAFFSFGALCVESVDKEMO
VLVSRIAAMMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLIGM
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Submitted (22-JUN-1993) Craig B Thompson, Howard Hughes Medical
Institute, University of Chicago, 5841 South Maryland, Chicago, IL,
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Primates; Catarrhin!; Hominidae; Homo.
1 (bases 1 to 926)
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PRI
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/db_xref="G1:510901"
/db_xref="SWISS-PROT:007817"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/clone="bcl-xL"
/dev_stage="Adult"
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/gene="bcl-xL"
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/gene="bcl-xL"
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H.sapiens bcl-xL mRNA.
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bcl-xL gene.
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/translation="MSQSNRELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESE
AETPSAINDRSWHLADSPAVWGATGHSSSLDAREVIPMAANKQALREADERELRYR
RAFSDLTSQLHITPGTASPSPGOVPURELFROGVWWGRIVAFFSFGGALCVESYDKEMO
VLVSRTATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERRNRELTGM
                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa anti-apoptotic regulator Bcl-xL (bcl-xL) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-DEC-1999) Biochemistry, SUNY at Buffalo, 3435 Main Street, Buffalo, NY 14214-3000, USA Location/Qualifiers
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1 (bases 1 to 720)
Lee,T.L. and Canty,J.M.
PCR Cloning of a Porcine bcl-xL cDNA from Heart
Unpublished
2 (bases 1 to 720)
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gctgggcggacttcacagctctatacggggacggggccctggaggacgcacggcgtctgc
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/protein_id="AAF33212.1"
/db_xref="G1:6959767"
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Pred. No. 1.6e-21;
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/db_xref="taxon:9823"
/tissue_type="heart"
1. .720
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DEFINITION
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1 (bases 1 to 926)
Thompson, C.B., Boise, L.H. and Nunez, G.
Vertebrate apoptosis gene: compositions and methods Patent: US 5834309-A 6 10 NOV-1998;
Location/Qualifiers
                                                                                                                                         Indels
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                                                                                                                                         0; Mismatches 173;
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454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513
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hompson, C.B., Boise, L.H. and Nunez, G.
Vertebrate apoptosis gene: compositions and methods
Patent: US 5646008-A 5 08-JUL-1997;
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Pred. No. 1.2e-21;
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al Similarity 58.3%;
236; Conservative
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Direct Submission
Submitted (02-NOV-1994) J.A. Cruz-Reyes, National Institute of
Medical Research, NIMR/MRC Mill Hill, The Ridgeway Road, London NW7
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DLGSRALVEDLVRYKLCQRSLVPEPSGAASCALHSAMRAAGDEFEERFRQAFSEISTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IHVTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDW
MVTYLETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression of two Xenopus bcl-2-like
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                                                                                      90121 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGAGTGGAACCACTGGTGGGA 90180
                                                                  caggittccgacgaactittccaaggggccctaactggggccgtcttgtgggattcttt 300
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Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
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ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc
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/organism="xenopus laevis"
/db_xref="taxon:8355"
/dev_stage="28-30 (tailbud tadpole)"
/clone_lib="lambda ZapII:R1"
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/db_xref="G1:1334682"
/db_xref="SWISS-PROT:091827"
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African clawed frog.
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Cruz-Reyes, J.A.
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X82462.1 GI:575421
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Score 233.8; DB 4; Length 749; Pred. No. 1.2e-44;

40.2%;

Query Match Best Local Similarity

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/translation="MSSSNRELVIDEVSYKLSQRGHCWSELEEEDENRTDTAAEAEMD SVLNGSPSWHPPAGHVVNGATVHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFS
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                                      aggeceageegeegeegetgeaceageeatgeggetgetggagaegagtttgagae 164
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Mismatches 152;
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/ Organism="Gallus gallus"
/strain="Hubbard White Mountain"
/db_xref="taxon:9031"
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Gallus gallus bcl-x mRNA, complete cds.
U26645
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/db_xref="G1:1522679"
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170. .859
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170. .859
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/note="matching EMBL:R59134; Identified using the e-PCR
software (G. Schuler)"
138504. .138653
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/note="matching EMBL:N91549; Identified using the e-PCR
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107991. 108176
/standard_name="D11677"
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128383. .128521
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/note="matching EMBL:AA167748; Identified using the software (G. Schuler)"
82162. .82297
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Pred. No. 2.9e-75;
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107753. 107946
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software (G. Schuler)"
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                                              /standard_name="H79035"
/note="matching EMBL:H79035; Identified using software (G. Schuler)"
93575. .93803
/standard_name="AA007328"
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/note="matching EMBL:R87257; Identified using
software (G. Schuler)"
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/note="matching EMBL:M78986; Identified
software (G. Schuler)"
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128415. .128539
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IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNS0000B 196287 bp DNA PRI 27-OCT-1999
Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-124D2 of
RPCI-11 library from chromosome 14 of Homo sapiens (Human),
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80431. .80564
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                           ccyctycaccaayccatycygyctyctygagacyaytttyagacccytttccyccycacc 180
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Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/db_xref="taxon:9606"
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78257. .78396
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<pre>Qy 481 cgtctgcgggaggcaactgggcatgagtgagcactgfgcgtggcgtg</pre>	Qy 541 ggggcctggtaactgtagggcctttttgctagcaatg 581 	RESULT 6 D87461 LOCUS D87461 3542 bp mRNA D87461 B7461 3542 bp mRNA ACCESSION VERSION VERSION VERSION SOURCE HOMO Sapiens CLOCUS ORGANISM HOMO Sapiens REFERENCE Tibates: Chararthini; Hominidae; Homo. REFERENCE Tibates: Chararthini; Hominidae; Homo. REFERENCE Tibates: Chararthini; Hominidae; Homo.		unpublished (1996) 3 (sites) 3 (sites) Nagase_T., Seti,N., Ishikawa,K., Ohira,M., Kawaraba, Nagase_T., Tanaka,A., Kotani,H., Miyajima,N. and Nom Prediction of the coding sequences of unidentified of The coding sequences of 80 new genes (KIAAQ201-KIAA) analysis of cDNa clones from cell line KG-1 and bra DNA Res. 3 (5), 321-329 (1996)	ψ O	gene 177758 CDS /gene="KlAA0271" CDS /gene="KlAA0271" /gene="KlAA0271" /noce="similar to human transforming protein bcl-2 (A24428)" /codon_start=1 /grotein_id="BAA19666.1" /db_xref="GI:1944418".1" /db_xref="GI:1944418".1" /ABAAGDEFETRFRRTFSDLAAQLHVTPGSAQORFTQVSDELFQGGPAADPLHQ /ARAAGDEFETRFRRTFSDLAAQLHVTPGSAQORFTQVSDELFQGGPNWGRLVAFFVF GAALCAESVNRREPELVGQVQBRWAYALLERTLADWIHSSGGWAEFTALYGDGALEEAR RIBEGWANASVRPVITGRAYALGAINTYNGAFFARR	BASE COUNT 804 a 817 c 1030 g 891 t ORIGIN Query Match 86.5%; Score 502.6; DB 9; Length 3542; Best Local Similarity 91.6%; Pred: No. 3.6e-107; Matches 532; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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/note="promotes cell survival"
                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/map="14011"
                                                                                                                                                                                                                                                                                                          /protein_id="AAB09055.1"
/db_xref="G1:1572493"
                                                                                                                                                                                                                                                                                                /product="Bcl-w"
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/gene="bcl-w"
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/gene="bcl-w"
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Direct Submission
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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Guastella, J.
Genes coding for bcl-y a bcl-2 homologue
Patent: US 5789201-A 1 04-AUG-1998;
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                                                                                                                         Location/Qualifiers
                                                                                                                                             /organism="unknown"
157 c 198 q
Sequence 1 from patent US
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95.9%;
                       AR020779.1 GI:3975394
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/translation="MATPASAPDTRALVADFVGYKLRQKGYVGAGFGEGPAADPLHQ
AMRAAGDEFETRERRFESDLAAQLHYPGSAQQRFTQYSDELFQGGPNWGRLVAFFVF
GAALCAESVNKEMEPLYGQVOEWMVAYLETRLADWIHSSGGNAEFTALYGDGALEBEAR
RLREGNWASVRTVLTGAVALGALYTVGAFFASK"
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Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 582)

Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G., Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S. bcl-w, a novel member of the bcl-2 family, promotes cell survival Oncogene 13 (4), 665-675 (1996)
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Hammer.S., Skoglosa,Y. and Lindholm,D.
Direct Submission
Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala
                                                                                                                                                     Length 3476;
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 582)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF096291 582 bp mRNA ROD 1
Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.
AF096291
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       /note="mRNA destabilization element" 3428. 3441
/gene="Bc1-w" 875 t
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                                                                    Score 560.2; DB 12
Pred. No. 1.5e-120;
0; Mismatches 13;
/gene="Bcl-w"
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Best Local Similarity 97.8
Matches 568; Conservative
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Rattus norvegicus
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Rlregnwasvrtvitgavalgalvtygaeffask"
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Pred. No. 1e-116;
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Uppsala 751 23,
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                                                                                                                                                                                      /gene="bcl-w"
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Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
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Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. Obcogene 13 (4), 665-675 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia Location/Qualifiers
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/gene="bcl-w"
/note="promotes cell survival; Bcl-2 homolog"
                                                     MMUS9746 582 bp mRNA ROD
Mus musculus Bcl-w (bcl-w) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_line="BaF3"
1. .582
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caagtccaggattggatcgtggcctacctggagacacgtctggctgactggatccacagc 420
                                                                             agiggcggctggggggacttcacagctctatacggggacggggccctggaggacgcacgg 480
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3476)
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Submitted (21-OCT-1997) Center for Molecular Medicine, Emory
University, 1462 Clifton Road, Atlanta, GA 30322, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      AF030769 3476 bp mRNA ROD
Mus musculus BCL-W (Bcl-W) mRNA, complete cds.
AF030769
                                                                                                                                                                                                                                                                                               Bcl-w is required for testis homeostasis Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAB86430.1"
/db_xref="GI:2623250"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/chromosome="14"
/map="19.5 cM"
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Ross, A.J. and MacGregor, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/10J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="BCL-W"
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/gene="Bcl-w"
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/gene="Bcl-w"
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/gene="Bcl-w"
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3356. .3364
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model
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July 4, 2000, 01:21:54; Search time 888.39 Seconds (without alignments)
-636.198 Million cell updates/sec Run on:

1 atgeegaceceageeteaac......geetttttgetageaagtg 581 US-09-155-327B-8 581 Title: Perfect score: Sequence:

882769 seqs, -486395729 residues Searched:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

1765538 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database :

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45:	46:	47:	48:	49:	50:	51:	52:	53:	54:	55:	56:	57:	58:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Mus musc	AF030769 Mus muscu	AF096291 Rattus no	AR020779 Sequence	Ξ	D87461 Human mRNA	AR020780 Sequence	AL049829 Human chr	.laevis R	U26645 Gallus gall	Seque	equer	•	Sns	ns sc	ttus	U72350 Rattus norv	norve	U34964 Rattus norv	ttu	ž.	man B		81	Ω.	M.musculus		TE1220 Mus musculu	ภัก เกิด	AR052622 Seguence	Sequence	AR052621 Sequence	80	H	I08038 Sequence 1	Human bc	24	0	60	7 H.	Ċ	054019	010 Sequence	U72349 Rattus norv
SUMMARIES	ID	MMU5974		AF0962	AR020779		D87461	AR020780		XLR1	GGU26645	7	152011	HSBCLXL	AF216205	٠,								AC016218				MMOTOTOL		AFORDS	AR052622	1	AR052621	AR054008	HUMBCL2A	I08038	HUMBCL2C	RATBCL2A	AR021160	AR054009	HSBCL2IG		R054	_	RNU72349
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ALIGNMENTS

US-09-155-327B-9.rsp

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                                                                                                                                                                                                                                                                                                82 GDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIASSLFESGINWGRVVALLGFSYRLALH 141
                                                                                                                                                                                                                                                                                                                 Query Match 16.9%; Score 234; DB 1; Length 211;
Best Local Similarity 31.5%; Pred. No. 2.28e-26;
Matches 34; Conservative 28; Mismatches 44; Indels 2; Gaps
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BH1.
BH2.
POTENTIAL.
FOTENTIAL.
W; 703875EC4DCCCID3 CRC64;
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                                                  EMBL; U16812; AAA74467.1; -. HSSP; Q16611; 1BXL. PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS050062; BCL2_FAMILY; 1. PFAM; PF04652; BC1-2; 1. Apoptosis; Transmembrane.
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117 136 BH1
169 184 BH2
189 205 POT
211 AA; 23411 MW; 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SÜBCELLULAR LOCATION: MEMBRANE-BOUND (POTENTIAL).
-!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
HIGHEST LEVELS IN THE HEART AND SKELETAL WISCLE.
-!- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK AND BAX FOR
THEIR KILLING ACTIVITY AND FOR THEER INTERACTION WITH ANTI-
APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                  Chittenden T., Harrington E.A., O'Connor R., Flemington C., Lutz R.J., Evan G.I., Guild B.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulators of apoptosis.";
Science 275:983-986(1997).
-I- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG EIB 19K PROTEIN.
-I- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, EIB 19K PROTEIN, AND BCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J., Elangovan B., Chinnadurai G., Lutz R.J.;
"A conserved domain in Bak, distinct from BH1 and BH2, mediates cell death and protein binding functions.";

EMBO J. 14:5589-5596(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Modulation of apoptosis by the widely distributed Bcl-2 homologue
                                                                                                                                                                                                               Farrow S.N., White J.H.M., Martinou I., Raven T., Pun K.-T., Grinham C.J., Martinou J.C., Brown R.; "Cloning of a bcl-2 homologue by interaction with adenovirus E1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 97172562.
Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E., Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J., Thompson C.B., Feslik S.W.;
Thompson C.B. Feslik S.W.;
"Structure of Bcl-xL-Bak peptide complex: recognition between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 95231654.
Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
Tomei L.D., Barr P.J.;
01-NOV-1997 (Rel. 35, Last annotation update)
BCL-2 HOMOLOGOUS ANTAGONIST/KILLER (APOPTOSIS REGULATOR BAK).
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eguchi H., Hayashi S.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                       "Induction of apoptosis by the Bcl-2 homologue Bak."; Nature 374:733-736(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND FUNCTION OF BH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 96-206 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 374:736-739(1995).
                                                                                                                                                                                                                                                                                                 Nature 374:731-733(1995)
                                                                 Homo sapiens (Human)
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                                             BAK1 OR BAK.
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-I-DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK AND BAX FOR THEIR KILLING ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

-I-SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).

-I-SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).

-I-SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).

-I-SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 GDDINRRYDSEFQTMLQHLQPTAENAYEYFTKIATSLFESGINWGRVVALLGFGYRLALH 141
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-1- SUBUNIT: FORMS HETERODIMES WITH BCL-2, E1B 19K PROTEIN, AND BCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 GDEFETRFRFFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
1-NOV-1997 (Rel. 35, Last annotation 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 SVNKEMEPLVGQVQDWIVAY-LETRLADWIHSSGGWADFTALYGDGAL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 VYQHGLTGFLGQVTRFVVDFMLHHCIARWIAQRGGWVAALNL-GNGPI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 235; DB 1; Length 211
Pred. No. 1.42e-26;
26; Mismatches 45; Indels
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send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apoptosis; Transmembrane; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                         PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS50062; BH3; 1.
PROSITE; PS50062; BC12_FAMILY; 1.
PFAM; PF00452; BC1-2; 1.
                                                                                            EMBL; U23765; AAA93066.1; --
EMBL; U16811; AAA74466.1; --
EMBL; D88397; BAA13606.1; --
EMBL; D88396; BAA13606.1; JOINED.
                                                             EMBL; X84213; CAA58997.1; -.
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Matches 35; Conservative
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                                                                                                                                                                                                                           PDB; 1BXL; 29-OCT-97.
MIM; 600516; -.
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Q13014;
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SEQUENCE
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                                                                                                                                                                                   BAK PROTEINS, AND WITH BCL-K(S). HETERODIMERIZATION WITH BAX REQUIRES INTACT BH1 AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).

SUBCELLULAR LOCATION: WITOCHONDRIAL INNER AND OUTER MEMBRANES, AS WELL AS NUCLEAR ENVELORE AND ENDOPLASMIC RETICULOM.

ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY DIFFER AT THEIR C-TERMINAL BNDS.

TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.

DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                 -i- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS BECAUSE IT INTERFERS WITH THE ACTIVATION OF CASPASES BY PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 VATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 QGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADF 147
                                                                                                                                             GENERATION SUCH AS MITOCHONDRIA.
SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHK -> VGACLVE (IN ISOFORM BCL-2-BETA).
AA85EF6B0766BE0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS5006; BL12_FAMILY; 1.
PROSITE; PS01289; BH1; 1.
PROSITE; PS01289; BH2; 1.
PROSITE; PS01269; BH4_1; 1.
PROSITE; PS01269; BH4_1; 1.
PROSITE; PS00452; BH4_2; 1.
PROSITE; PS50063; BH4_2; 1.
PROSITE; PS50063; BH4_2; 1.
PROMITE; PS50063; BH4_2; 1.
PROMITE; PS50063; BH4_2; 1.
PROMITE; PS50063; BH4_2; 1.
BR00TCS1S; BC1-2; 1.
BR00TCS1S; BC1-2; 1.
BH4.
                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 554; DB 1; 1
Pred. No. 3.72e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
Nucleic Acids Res. 20:4187-4192(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, L31532, AAA37282.1; -.
EMBL, M16506; AAA37282.1; JOINED.
EMBL, M16506; AAA37281.1; -.
PIR, AZ5960; TVMSA1.
PIR, B25960; TVMSB1.
PIR, B37332, E3732, E3732,
HSSP; Q07817; IMAZ.
MGD; MGI:88138; BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 AA; 26425 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 40.0%;
Best Local Similarity 43.4%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                           <u>+</u>
                                                                                                                                                                                                                                                                                                    <u>+</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 GPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDMIVAXLETRLADWIHSSGGWADFTA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 GEGATQGIVEEEVLQALLEATEEFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRD 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 GINWGRIVAFFSFGRALCVESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVG 165
                                                                                                                                                                                                                                                                                      2; Gaps
                                                                                                                                                                                                                                                            Cruz-Reyes J., Tata J.R.; "Cloning, characterization and expression of two Xenopus bcl-2-like
                                                                                                                                  APOPTOSIS KEGULATOR KII (XKII).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48; Indels
148 TALYGDGALEDARRLREGNW-AVSTVVTGAVALGALVTVGAFFASK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 AA; 23379 MW; 3BFC6BE6DDA4CA03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 546; DB 1; 1
Pred. No. 2.78e-96;
                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Mismatches
                                                        204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAK_HUMAN STANDARD; PRT; 211 AA (16611; Q92533; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 LYGDGALEDARRIREG-NWAVSTVV-TGAVAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 LYGKNAAAQSRESQERFGRLLTIVMLTGVFAL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PSO1080; BH1; 1.
PROSITE; PSO1258; BH2; 1.
PROSITE; PSO0625; BCL2_FAMILY; 1.
PFAM; PF00452; BCl-2; 1.
Apoptosis; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BH1.
                                                                                                                              APOPTOSIS REGULATOR R11 (XR11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X82461; CAA57844.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 39.4%;
Local Similarity 46.7%;
les 71; Conservative
                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 TISSUE=HEAD;
MEDLINE; 95331613.
                                          T 13
AR11_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                        Xenopus.
                                                                       091828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                          ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA. SUBMUTE: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND BAK PROTEINS, AND WITH BCL. X(S). HETERODIMERIZATION WITH BAX AND REQUIRES INTACT BHI AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY.
                                                                                                                                                          Hockenbery D., Nunez G., Milliman C., Schreiber R.D., Korsmeyer S.J.; "BGL-2 is an inner mitochondrial membrane protein that blocks programmed cell death."; Nature 348:334-336(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ALSO KNOWN AS TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WELL AS NICLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.
-!- ALTERNATIVE PRODUCTS: TWO FORMS OF BCL-2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIFFER AT THEIR C-TERMINAL BNDS.
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      II CHRONIC LYMPHATIC LEUKEMIA) BY A CHROMOSOMAL TRANSLOCATION T(14;18)(Q32;Q21) WHICH INVOLVES BCL2 AND IMMUNOGLOBULIN GENE
                                                                                                                                                                                                                                                                                                                                                                            -1- FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOIETIC CELLS IN THE
MEDLINE; 92096610.

Tanaka S., Loule D.C., Kant J.A., Reed J.C.;

"Frequent incldence of somatic mutations in translocated BCL2 oncogenes of non-Hoddykin's lymphomas.";

Blood 79:229-237(1992).
                                                                                                                                                                                                                                                                        MEDILNE; 94239528.
Yin X.-M., Oltvai 2.N., Korsmeyer J.;
"BH1 and BH2 domains of Bcl-2 are required for inhibition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISEASE: INVOLVED IN FOLLICULAR LYMPHOMA (FL)
                                                                                                                                                                                                                                                                                                                                     apoptosis and heterodimerization with Bax."; Nature 369:321-323(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M13994; AAA51813.1; ALT_SEQ.
EMBL; M13995; AAA51814.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD14111.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X06487; CAA29778.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M14745; AAA35591.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B29409; TVHUB1.
A24428; TVHUBC.
C37332; C37332.
                                                                                                                     SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; D37332; D37332.
HSSP; P53563; lAF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A29409; TVHUA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50062;
                                                                                                                                      MEDLINE; 91066924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S72602;
                                                                                                                                                                                                                                                            MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGIONS
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/FTIG-VAK_000828.
V -> I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
MUTATION).
                                                                                                                   POTENTIAL.
DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
                                                                                                                                           GHK -> VGASGDVS (IN ISOFORM BCL-2-BETA).
G->A: NO HETERODIMERIZATION WITH BAX, AND
                                                                                                                                                                      DF ANTI-APOPTOTIC ACTIVITY.
NO HETERODIMERIZATION WITH BAX, AND
                                                                                                                                                                                                                        /FTId-VAR_000827.
P -> S (IN NON-HODGKINS-LYMPHOMA; SOMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 AAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLIPFTARGRFATVVEELFRD 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eguchi Y., Ewert D.L., Tsujimoto Y.; Isbuchi Y., Ewert D.L., Tsujimoto Y.; Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.; "Molecular analysis of mbol-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma."; Cell 49:455-463(1987).
          PFAM; PF00452; Bcl-2; 1.
Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane; Mitochondrion; Chromosomal translocation; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                LOSS OF ANTI-APOPTOTIC ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                           41; Indels
                                                                                                                                                                                                                                                                                                                 I -> F (IN REF. 4).
P -> T (IN REF. 3).
S -> R (IN REF. 3).
R -> C (IN REF. 4).
W; 3C49F2B714DC9CCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| :: | | :: | :: |: |: || :|| 150 LYGDGALEDARRLREGNW-AVSTVVTGAVALGALVTVGAFFASK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 LYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
                                                                                                                                                                                                                                                                                                                                                                                     t match 40.1%; Score 556; DB 1; l Local Similarity 43.3%; Pred. No. 1.27e-98; les 71; Conservative
                                                                                                                                                                                                                                                                                                MUTATION).
/FTId=VAR_000829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCL2_MOUSE STANDARD; PRT; 236 AA. P10417; P10418; 01-MAR-1989 (Rel. 10, Created) 01-APR-1993 (Rel. 25, Last sequence update) 15-UL-1998 (Rel. 36, Last annotation update) APOPTOSIS REGULATOR BCL-2.
                                                                                                                                                                                                                                                MUTATION
                                                                                                                                                                       Ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W->A:
                                                                                                                                                                       ross
                                                                                                                                                                                                                                                                                                                   48 I
59 P
117 S
129 R
26266 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/C; TISSUE-LIVER; MEDLINE; 87187643.
PROSITE; PS50063; BH4_2; 1.
                                                               30
107
155
202
233
233
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                                                                                                                                                                                                                                                                                                                   48
59
117
129
239 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                    Disease mutation
                                                                                                                                                        145
                                                                                                                                                                                                                                      59
                                                                                                                                                                                  188
                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                              93
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                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                   CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                VARSPLIC
                                                                                                                                                         MUTAGEN
                                                                                                                                                                                                                                                                              VARIANT
                                                                            DOMAIN
                                                                                                                                                                                   MUTAGEN
                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                       VARIANT
                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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splicing; Transmembrane; Mitochondrion

Alternative

Apoptosis;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERATION SUCH AS MITCCHOURIA.

SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND BAX PROGRESS. THE SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX REQUIRES INFACT BH1 AND BH2 DOMAINS, AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).

SUBCELLULAR LOCATION: MITCGHONDRIAL INNER AND OUTER MEMBRANES, AS WELL AS WOLLEAR ENVELOPE AND ENDOPLASMIC RETICULUM.

ALTERNATIVE PRODUCTS: TWO FORMS OF BCL. 2: ALPHA, AND BETA, ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY ONLY
                                                                                                                                               STRAIN-SPRAGUE-DWALEY, TISSUE-OVARY,
MEDLINE; 95120487.
Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
FEXPRESSION of members of the bcl-2 gene family in the immature rat
ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
cell apoptosis is associated with decreased bax and constitutive
bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BECAUSE IT INTERFERES WITH THE ACTIVATION OF CASPASES BY PREVENTING THE RELEASE OF CYTOCHROME C. MIGHT FUNCTION IN AN ANTIOXIDANT PATHWAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRANULE AND PYRAMIDAL NEURONS OF HIPPOCAMPUS, PONTINE WICLET, CEREBELLAR GRANULE NEURONS, AND IN EPENDYMAL CELLS. IN PRENATAL BRAIN, EXPRESSION IS HIGHER AND LOCALIZED IN THE NEUROEPITHELIUM AND IN THE CORTICAL PLATE.
                                         Sato T., Irie S., Krajewski S., Reed J.C.; "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein."; Gene 140:291-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: PROLONGS THE SURVIVAL OF HEMATOPOLETIC CELLS IN THE ABSENCE OF REQUIRED GROWTH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                           'bcl-2 messenger RNA is localized in neurons of the developing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIFFER AT THEIR C-TERMINAL ENDS.
TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES, WITH
HIGHEST LEVELS IN REPRODUCTIVE TISSUES. IN THE ADULT BRAIN,
EXPRESSION IS LOCALIZED IN MITRAL CELLS OF THE OLFACTORY BULB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                        Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50062; BCL2_FAMILY; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS01259; BH3; 1. PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1. PROM; PF00452; BCl-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neuroscience 61:165-177(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L14680; AAA53662.1; -.
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 19-172 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; S74122; CAB33200.1; -. HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U34964; AAA77687.1; -
                    MEDLINE; 94193015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adult rat brain.";
                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                            95059917
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  LISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                        Lindholm D.;
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Eguchi Y., Ewert D.L., Tsujimoto Y.; "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in
                                                                                                                                                                                                                      76 VANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
                                                                                                                                                                                                                                                                             136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
                                                                                                                                                                                                                                                                                            MEDLINE; 87002488.
Cleary M.L., Smith S.D., Sklar J.;
"Cloning and structural analysis of CDNAs for bc1-2 and a hybrid bc1-
2/immunoglobulin transcript resulting from the t(14;18)
                                                                                                                                                                                                                                    28 VCGAGPGECPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELF 87
                                                                                                                                                                                            6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-1g fusion gene in lymphoma."; EMBO J. 7:123-131(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsujimoto Y., Croce C.M.;
"Analysis of the structure, transcripts, and protein products of bol-2, the gene involved in human follicular lymphoma.";
Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-131 FROM N.A., AND VARIANTS NON-HODGKINS-LYMPHOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,
                                                                                                                                                                DB 1; Length 236;
                                                                                                                                                                                            45; Mismatches 43; Indels
                                                                             A -> R (IN REF. 2).
E -> G (IN REF. 1).
S -> Y (IN REF. 2).
L -> O (IN REF. 2).
W; E7688CB9071A872A CRC64;
                                                                                                                                                                                                                                                                                                                                   196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
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01-MAR-1989 (Rel. 10, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                    239 AA
                                                                                                                                                      Score 556; D
                                                                    POTENTIAL.
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                                                                                                                         212 I
26622 MW;
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                                                                                                                                                                             Local Similarity 43.4%;
nes 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APOPTOSIS REGULATOR BCL-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                        104
152
199
230
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                                     133
184
209
42
157
164
212
236 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adult and embryo."
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BCL2_HUMAN
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CONFLICT
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SEQUENCE
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           DOMAIN
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"Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue of the Bol-2 oncoprotein."

"Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue of the Bol-2 oncoprotein."

"Biochim. Biophys. Acta 1132:109-113(1992).

"I BIOCHIM. BIOPHYS. ACTA 1132:109-113(1992).

"I BIOCHIM. BOOM THE RELATION OF CASPASES BY ARROUGH FACTORS AND ALSO IN THE PRESENCE OF VARIOUS STIMULI INDUCING CELLULAR DEATH. BCL2 BLOCKS APOPTOSIS BECAGNES IT INTERFERES WITH THE ACTIVATION OF CASPASES BY PREVENTING THE RELASE OF CYTOCHROME C. MIGHT FUNCTION IN AN ANTIOXIDARY PARHAY TO PREVENT APOPTOSIS AT SITES OF FREE RADICAL GENERATION SUCH AS MITOCHONDRIA (BY SIMILARITY).

"SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BAX AND BAX PROTEINS. HETERODIMERIZATION WITH BAX REQUIRES INTACT BHI AND BAX AND CONTERNS. HETERODIMERIZATION WITH BAX REQUIRES INTACT BHI AND CONTENT AND IS NECESSARY FOR ANTI-APOPTOTIC ACTIVITY (BY CONTENT AND CONTENT 
                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eguchi Y., Ewert D.L., Tsujimoto Y.; "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo."; Nucleic Acids Res. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                    85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVLNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                       145 SFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                                          101 VFGAALCAESVNKEMEPLVGGVQDMIVAYLETRLADMIHSSGGWADFTALYGDGALEDAR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
SUBCELLUIAR LOCATION: MITOCHONDRIAL INNER AND OUTER MEMBRANES, AS
WELL AS NUCLEAR ENVELOPE AND ENDOPLASMIC RETICULUM (BY
                                                                                                                                                                                                                                                            3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-i- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                                                                                                                                                                                                      Score 613; DB 1; Length 233;
Pred. No. 4.92e-112;
35; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
                                                                                                                                                                                    18BF6FA0441912B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
APPPPOSIS REGULATOR BCL'-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 AA.
                                                       PFAM; PF00452; Bcl-2; 1.
Apoptos1s; Mitochondrion; Transmembrane.
                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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161 RLREG-N-WAVSTV-VTGAVALGAL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                               205 KGQERFNRWFLTGMTLAGVVLLGSL 229
                                                                                                                                 BH1
                                                                                                        86 100 BH3
129 148 BH1
180 195 210
210 226 POT
233 AA; 26061 MW; 1
BH3; 1.
BH4_1; 1.
BH4_2; 1.
                                                                                                                                                                                                                      Query Match
Best Local Similarity 51.7%;
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCL2 OR BCL-2.
Gallus gallus (Chicken).
                   PS01260; 1
PS50063; 1
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 PS01259;
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Q00709;
                                                                                                                                                                   TRANSMEM
SEQUENCE
   PROSITE;
                    PROSITE;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 PAPAAAPAAVAAAGASSHHRPEPPGSAAASEVPPAEGLRPAPPGVHLALRQAGDEFSRRY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 ORDFAOMSGOLHLIPFTAHGRFVAVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 LVDNIATWMTEYLNRHLHNWIQDNGGWDAFVELYGN-SM---RPLFDFSWISLKTILSLV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 561; DB 1; Length 233; Pred. No. 8.52e-100;
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5252555ACB6E4C3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E -> S (IN REF. 2).
GSAAASEVPPAEGLRP ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IN REF. 2).
H -> T (IN REF. 2).
G -> V (IN REF. 2).
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                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptosis; Transmembrane; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH2.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S24350; 1.1. HSSP, P53653; 1AF3, PROSITE; PS50062; BCL2_FAMILY; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                             EMBL; D11382; BAA01978.1; -.
EMBL; D11381; BAA01978.1; JOINED.
EMBL; Z11961; CAA78018.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1. PFAM; PF00452; Bcl-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 LVGACITLGAYLGHK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|| :|:||::|
178 ALGALVTVGAFFASK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30
101
149
196
228
64
82
                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A37332; A37332.
PIR; S24390; S24390.
HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 ]
233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
101 VFGAALCAESVNKEMEPLVGQVQDMIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T., Turka L.A., Mao X., Nunez G., Thompson C.B.; "bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOI. REPLOG. DEV. 47:26-29(1997).

-1- FUNCTION: DOMINNIT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (BY SIMILARITY).

-1- ALTERNATIVE PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT ISOFORM ARE PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT ISOFORM ARE PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT ISOFORM ARE PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT ISOFORM ARE PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT ISOFORM ARE PRODUCTS: A LONG ISOFORM (SHOWN HERE) AND A SHORT ISOFORM ARE PRODUCTS: A LONG ISOFORM AND A SHORT ISOFORM AND A SHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vilagrasa X., Mezquita C., Mezquita J.;
"Differential expression of bcl-2 and bcl-x during chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                           BCLX_CHICK STANDARD; PRT; 229 AA. 007815; 098908; 01-FEB-1995 (Rel. 31, Created) 11-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-HUBBARD WHITE MOUNTAIN; TISSUE-TESTIS; MEDLINE; 97264485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50062; BCL2 FAMILY; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01289; BH2; 1. PROSITE; PS01259; BH3; 1. PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1.
                                                                                 205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                 ::| | |:::| ||:|:
161 RLREG-N-WAVSTV-VTGAVALGAL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (SHORT FORM). MEDLINE; 93364977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2] SEQUENCE FROM N.A. (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z23110; CAA80657.1; -. EMBL; U26645; AAB07677.1; -.
                                                                                                                                                                                                                                                                                                                                                                                      APOPTOSIS REGULATOR BCL-X.
BCL2L1 OR BCLX OR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 74:597-608(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A47537; A47537.
HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00452; Bcl-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spermatogenesis.
Mol. Reprod. Dev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
ERFVDLYGNNAAAELRKGQETFNKWLLTGATVAGVLLIGSL
                                                                                                                                                                                                                                                                   79 ASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFHDGVNWGRIVA 138
                                                                                                                                                                                                                                                   139 FFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDPWIQENGGWERFVDLYGNNAAAE 198
                                                                                                                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.; "Expression of apoptosis-associated genes in hibernating and stunned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (BY SIMILARITY).
DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION: INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).
                                                                                     LSRK -> VRTALP (IN SHORT ISOFORM)
A97D3A4D04C0E9DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                            36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                  Length 229;
                                                                                                                                  Score 620; DB 1; Le Pred. No. 1.09e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                              , Last sequence update)
, Last annotation update)
                                                                                                                                                               33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     233 AA
                                                                                                                                                                                                                                                                                                                              |: :| | | : : |:| : |:|:| | 159 ARRLREG-N-WAVS-TVVTGAVALGALVT 184
                                                                                                                                                                                                                                                                                                              199 LRKGQETFNKWLLTGATVAGVLLLGSLLS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ001203; CAA04597.1; -. PROSITE; PS50062; BRL2 FAMILY; 1. PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
                                                                                                   229 AA; 25733 MW;
                                                                                                                               Match 44.7%;
Local Similarity 51.7%;
es 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APOPTOSIS REGULATOR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCL2L1 OR BLC2L OR BCLX.
24
96
144
191
223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
 82
125
176
206
185
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                                                                                                                                                                                                                                                                                                                                                                                    LT 8
BCLX_PIG
077737;
                                            DOMAIN
TRANSMEM
                                                                                                   SEQUENCE
                                                                                                                                Query Match
                                                                        VARSPLIC
                             DOMAIN
                DOMAIN
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                                                                                                                                                                                                               145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N., Ohta S., Seldin M.F., Nunez G.;
"Genomic organization, promoter region analysis, and chromosome localization of the mouse bcl-x gene.";
"Immunol. 158:4750-4757(1997).
-!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG FORM AND THE DELTA-TM FORM DISPLAY CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT ISOFOWN PROMOTES APOPTOSIS (BY SIMILARITY).
-!- SUBBUIT: BCL-X(L) FORMS HETERODIMERS WITH BAX AND BAK, WHEREAS BCL-X(S) FORMS HETERODIMERS WITH BCL-2. HETERODIMERIZATION WITH
                                                                                                                85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                             3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fang W., Rivard J.J., Mueller D.L., Behrens T.W.; *Cloning and molecular characterization of mouse bcl-x in B and T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang X.-F., Weber G.F., Cantor H.;
aA novel Bel.x isoform connected to the T cell receptor regulates
appptosis in T cells.''
Immunity 7:629-639(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thompson C.B., Nunez G.; "bol-x mRNA form expressed during murine "bol-XL is the major bol-x mRNA form expressed during murine development and its product localizes to mitochondria."; Development 120:3033-3042(1994).
                                   44.9%; Score 623; DB 1; Length 233; 52.4%; Pred. No. 2.13e-114;
                                                                         34; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (X(L); X(S) AND X(DELTA-TM) ISOFORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=2A4B;
Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
233 AA; 26049 MW; E09D3CDD851AE9BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                               BCLX_MOUSE STANDARD; PRT; 233 AA. 064373 x 666378; 661338; 061073 x 666373 x 666378; 061388; 061-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS).
STRAIN-C57BL/6; TISSUE-BRAIN;
MEDLINE; 95331139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (BETA ISOFORM).
STRAIN-C57BL/6 X CBA; TISSUE-THYMUS;
MEDLINE; 98051053.
                                                                                                                                                                                                                                                                    205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                          lymphocytes.";
J. Immunol. 153:4388-4398(1994).
                                                       Best Local Similarity 52.4%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-PRE-B CELL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 95052604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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 SEQUENCE
                                       Query Match
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                                                                                                                                                                                                       -!- DEVELOPMENTAL STAGE: BCL-X(BETA)IS EXPRESSED IN BOTH EMBRYONAL AND POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN POSTNATAL TISSUES.
-!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY) ENGLASH BELL-2 HOMOLOGY DOMAIN 1 (BH1).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
MISSING (IN ISOFORM BCL-X(S)).
DTFYDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSRK -> VRTTPLVCPPLACVSLLCEHP (IN ISOFORM BCL-X-BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYGNNAAAESÄKGQERFNRWFLTGMTVAGVVLLGSLFSRK
-> GHDCGWCGSAGLTLQSEVTRH (IN ISOFORM BCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-TM) EXPRESSION IS ENHANCED IN B AND I LYMPHOCYTES THAT HAVE BEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 SFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
                                                        ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELFA-TM).
ALTERNATIVE PRODUCTS: FOUR ISOFORMS, BCX-X(L) (SHOWN HERE), BCL-X(S), BCL-X-BETA AND BCL-X(DELTA-TM), ARE DERIVED BY ALTERNATIVE
BAX DOES NOT SEEM TO BE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Gaps
                                           SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.9%; Score 623; DB 1; Length 233; 52.4%; Pred. No. 2.13e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24D2AC79887E072E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X(DELTA-TM))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB96881.1; -...AAB96881.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 AA; 26132 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, U10102, AAA82174.1;
EMBL, U10101, AAA82173.1;
EMBL, U10100; AAA82172.1;
EMBL, U51279; AAC53460.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X83574; CAA58557.1; -. EMBL; L35049; AAA51039.1; -. EMBL; L35048; AAA51040.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
PFAM; PF00452; Bcl-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 52.4%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCL2L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:88139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194
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U78030;
                                                                                                                                                                                             ACTIVATED
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
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Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B., Korsmeyer S.J.;
"Multiple Bcl-2 family members demonstrate selective dimerizations with Bax.";
                                                                                                                                                                                                                                                            85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
                                                                                                                                                                                                                                             145 SFGGALCVESYDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NWR OF 1-209.
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).

BEDLINE; 93364971.

Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
Turka L.A., Mao X., Nunez G., Thompson C.B.;

First D.A., Mao X., Nunez G., Thompson C.B.;

JASOI-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.";

Cell 74:597-608(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheng E.H.-Y., Levine B., Bolse L.H., Thompson C.B., Hardwick J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 97172562.
Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,
Sattler M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
Thompson C.B., Fesik S.W.,
Thompson C.B. Resik S.W.,
"Structure of Bcl-xL-Bak peptide complex: recognition between
regulators of apoptosis.";
Science 275:983-986(1997).
                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                Score 623; DB 1; Length 233;
                                                                                                                                               34; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (BETA ISOFORM).
Inohara N., Ohta S.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                2B62B6C63864BC8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Bax-independent inhibition of apoptosis by Bcl-XL.";
 I -> L (IN REF. 4).
A -> V (IN REF. 4).
FF -> SS (IN REF. 4).
A -> T (IN REF. 4).
A -> P (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
                                                                                                                              Pred. No. 2.13e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                        BCLX_HUMAN STANDARD; PRT; 233 AA. 207817; 092976; Christope (PEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                           205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                              ::| | | ::: |:| | ||:| RLREG-N-WAVSTV-VTGAVALGAL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUTAGENESIS OF BH1 AND BH2 DOMAINS
81
119
144
199
201
26158 MW;
                                                                                                               44.98;
52.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 1-209.
                                                                                                                                               76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                 Best Local Similarity
                                                                               233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 96170038.
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                  CONFLICT
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SEQUENCE
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   CONFLICT
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                                                                                                                                                                     CHIL GEALL. "SELLONG"

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DTFVELYGNNAAAESERGGERFNRWFLTGWYAGVYLLGSL
FSRK -> VRYKPLVCPFSLASGGRSFTALLLYLFLLCWVI
FYGUDG (IN ISOFORM BCL-X(BETA)).
FRD->VRA: NO HETERODLMERIZATION WITH BAX.
VNW->AIL: LOSS OF ANTI-APOPTOTIC
                      Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
Yoon H.S., Nettesheim D., Chang B.S., Thompson C.B., Wong S.L.,
Ng S.L., Fesik S.W.;
"X-ray and NMR structure of human Bcl-xL, an inhibitor of programmed
cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY BY ABOUT HALF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R EMBL; 223115; CAA80662.1; -
R EMBL; 223115; CAA80661.1; -
R EMBL; 223115; CAA80761.1; -
R PDB; 1LXL; 21-APR-97.
R PDB; 1LXL; 21-APR-97.
R PDB; 1LXL; 21-APR-97.
R PDB; 1LXL; 21-APR-97.
R PROSITE; PS01060; BH1; 1.
R PROSITE; PS01259; BH2; 1.
R PROSITE; PS01259; BH3; 1.
R PROSITE; PS01260; BH4.1; 1.
R PROSITE; PS01250; BH4.1; 1.
R PROSITE; PS01260; BH4.1; 1.
R PROS
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148
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MEDLINE; 96256675
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G -> A (IN CAA80661).

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                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 LETRLADWIHSSGGWADFTALYGDGALEDARRLREGNWA-VSTVVTGAVALGALVTVGAF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 VTPGTAXARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWAVTY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 LETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 SRALVEDLVRYKLCQRSLV--PEPS-GAASCALHSAMRAAGDEFEERFRQAFSEISTQIH 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohta S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wesselingh S.L., David G.L., Choi S., Veliuona M., Hardwick J.M.; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 96278736.
Shiralwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Oh
"An additional form of rat Bcl-x, Bcl-xbeta, generated by an
unspliced RNA, promotes apoptosis in promyeloid cells.";
                                                                                                                                                                                                                                                                                                                                                                                               Length 228;
                                                                                                                                                                                                                                                                                                                                                                                          Score 900; DB 1; Length 228, Pred. No. 9.34e-181; 36; Mismatches 22; Indels
-i- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCLX RAT STANDARD; PRT; 233 AA. PSCA. RAT STANDARD; P70613; Q62836; Q64087; Q64128; Q1-0CT-1996 (Rel. 34, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                139 BH1.
186 BH2.
227 POTENTIAL.
25068 MW; C499D449A585F8A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (X(L) AND BETA ISOFORMS).
                                                                                                                                                                                                            PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
PFAM; PF00452; BC1-2; 1.
                                                                                                                                                                                 EMBL; X82462; CAA57845.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            Watch 64.9%;
Local Similarity 66.3%;
hes 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APOPTOSIS REGULATOR BCL-X.
BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                   Apoptosis; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                              120 1
171 1
207 2
228 AA;
                                                                                                                                                                                                P53563; 1AF3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-THYMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 FASK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 FASK 192
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SEQUENCE
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DOMAIN
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MISSING (IN ISOPORM BCL-X(S)).

DIFYDLYGRONAAAESRKGOEFNRWFLTGWTVAGVVLLGSL

FSRR -> VRTPLVCPPLVCLSSVBIPNCPFWSEGMVVED

IDYSGDIPGLL (IN ISOFORM BCL-X(BETA)).

F -> Q (IN REF. 1).

A -> E (IN REF. 2).
                                                                                                                          SIMILARITY).

C -: SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (BY SIMILARITY).

C -: ALTERNATIVE PRODUCTS: THREE ISOCORMS, BCL-X(L) (SHOWN HERE), BCL-X(S) AND BCL-X(S) THREE ISOCORMS. BCL-X(L) (SHOWN HERE), C -: TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT DETECTABLE LEVEL OF BCL-X(S).

C -: DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).

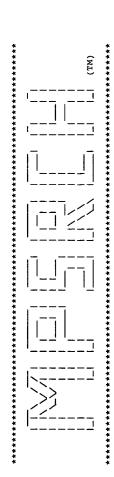
C -: SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).

C -: SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 3 (BH3).

C -: SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
                                              SEQUENCE FROM N.A. (X(L) AND X(S) ISOFORMS).
STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY;
MEDLINE; 95129487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X82537; CAA57886.1; -.
EMBL, X82537; CAA57887.1; -.
EMBL, 10579; AAA19257.1; -.
EMBL, U72350; AAB17353.1; -.
EMBL, U72349; AAB17353.1; -.
EMBL, U72349; AAB17352.1; -.
EMBL, S76513; AAA77686.1; -.
EMBL, S76513; AAC60701.1; ALT_INIT.
EMBL, S78284; AAC60702.1; -.
J. Biol. Chem. 271:13258-13265(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50062; BCL2_FAMILY; 1. PROSITE; PS01060; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS01259; BH3; 1. PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1.
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148
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226
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64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86
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  REAL PROPERTY AND DESCRIPTION OF THE PROPERTY AND DESCRIPTION
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-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND
IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
                                                                                                                                                                                                                                                                                                                                                                                                                            61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                   61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G., Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.; bcl-w, a novel member of the bcl-2 family, promotes cell survival."; Oncogene 13:665-675(1996).
                                                                                                                                                                                                                                                                                                   1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain."; DNA Res. 3:321-329(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                      Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                       36CA185F5945DFB4 CRC64;
                                                                                                                                                                                                                                     97.0%; Score 1345; DB 1; 1
95.9%; Pred. No. 1.76e-289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    092843;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BCL2L2 OR BCLW.
                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: PROMOTES CELL SURVIVAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                        MGD; MGI:108052; BCLZLZ.
PROSITE; PS50062; BCLZ_FAMILY; 1.
PROSITE; PS611080; BH1; 1.
PROSITE; PS61258; BH2; 1.
PROSITE; PS61250; BH4_1; 1.
PROSITE; PS51250; BH4_2; 1.
PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                       9 29 BH
85 104 BH
136 151 BH
193 AA; 20790 MW;
EMBL; AF030769; AAB86430.1;
HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                      185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 GALVTVGAFFASK 192
                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 96358615.
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                                                                                                                                            Apoptosis.
                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARI_XENLA STANDARD; PRT; 228 AA.
091827; 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
APOPTOSIS REGULATOR RI (XRI) (FRAGMENT).
Xenopus laevis (African clawded frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 193;
SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4). SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3792243A50281761 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1341; DB 1; Pred. No. 1.70e-288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Mismatches
                                                                                                                                                                                                                                                                                                   EMBL; U59747; AAB09055.1; -.
EMBL; D87461; BAA19666.1; -.
HSSP; P53563; 1AF3.
MIM; 601931; -.
PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01260; BH2; 1.
PROSITE; PS01260; BH4_1; 1.
PROSITE; PS0063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH4
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104 BH
151 BH
; 20774 MW;
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Local Similarity 94.8%;
les 183; Conservative
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DOMAIN
SEQUENCE
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protein · protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Jun 23 14:18:44 2000; MasPar time 8.06 Seconds 725.519 Million cell updates/sec Run on:

Tabular output not generated

(1-192) from US09155327B.pep 1386 >US-09-155-327B-9 Description: Perfect Score:

1 MPTPASTPDTRALVADFVGY......VTGAVALGALVTVGAFFASK 192 Sequence:

Scoring table:

83857 seqs, 30454973 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot38 1:swissprot Database:

Mean 45.917; Variance 78.366; scale 0.586 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query	1	á	ŕ		·	ć	
9	score	Match	Length	e :	1.0	Description		¥ :	rred. NO.
П	1345	97.0	193	7	BCLW_MOUSE	APOPTOSIS 1	REGULATOR B	S	1.76e-289
7	1341	96.8	193	٦	BCLW_HUMAN	APOPTOSIS	REGULATOR B	BC	1.70e-288
က	006	64.9	228	-	AR1_XENLA	APOPTOSIS 1	REGULATOR R	2	9.34e-181
4	623	44.9	233		BCLX_RAT	APOPTOSIS 1	REGULATOR B	BC	2.13e-114
Ŋ	623	44.9	233	Н	BCLX_HUMAN	APOPTOSIS 1	REGULATOR B	ည္ထ	2.13e-114
9	623	44.9	233	-	BCLX_MOUSE	APOPTOSIS 1	REGULATOR B	S B	2.13e-114
7	620	44.7	229	-	BCLX_CHICK	APOPTOSIS 1	REGULATOR B	BC	1.09e-113
æ	613	44.2	233	Н	BCLX_PIG	APOPTOSIS 1	REGULATOR B	BC	4.92e-112
σ	561	40.5	233	~	BCL2_CHICK	APOPTOSIS 1	REGULATOR B	BC	8.52e-100
10	556	40.1	236	~	BCL2_RAT	APOPTOSIS 1	REGULATOR B	BC	1.27e-98
11	556	40.1	239	Н	BCL2_HUMAN	APOPTOSIS 1	REGULATOR B	BC	1.27e-98
12	554	40.0	236	Н	BCL2_MOUSE	APOPTOSIS 1	REGULATOR B	BC	3.72e-98
13	546	39.4	204	Н	AR11_XENLA	APOPTOSIS 1	REGULATOR R	R1	2.78e-96
14	235	17.0	211	-1	BAK_HUMAN	BCL-2 HOMO]	HOMOLOGOUS ANTAG	Į.	1.42e-26
15	234	16.9	211	Н	BAK2_HUMAN	BCL-2 HOMO]	HOMOLOGOUS ANTAG	ģ	2.28e-26
16	229	16.5	192	-	BAXA_RAT	APOPTOSIS 1	REGULATOR B	BA	2.45e-25
17	229	16.5	192	-	BAXA_MOUSE	APOPTOSIS 1	REGULATOR B	BA	2.45e-25
18	227	16.4	192	٦	BAXA_BOVIN	APOPTOSIS 1	REGULATOR B	BA	6.32e-25
19	226	16.3	143	Н	BAXD_HUMAN	BAX PROTEIL	BAX PROTEIN, CYTOPLASM	×	1.01e-24
20	226	16.3	192	-	BAXA_HUMAN	APOPTOSIS I	REGULATOR B	BA	1.01e-24
21	215	15.5	218	-	BAXB_HUMAN	APOPTOSIS I	REGULATOR B	BA	1.77e-22
22	214	15.4	208	-	BAK_MOUSE	BCL-2 HOMOI	BCL-2 HOMOLOGOUS ANTAG	 g	2.83e-22
23	195	14.1	177	-	NR13_COTJA	APOPTOSIS I	REGULATOR N	E E	1.78e-18

4.51e-13	3.88e-12	1.40e - 11	9.12e-12	4.10e-07	6.09e-07	6.09e-07	2.03e-02	5.67e-02	1.55e-01	5.73e - 01	5.73e - 01	5.73e-01	7.89e-01	7.89e-01	1.08e+00	1.49e+00	2.03e+00	2.03e+00	2.03e+00	2.03e+00
BCL2-RELATED PROTEIN A	APOPTOSIS REGULATOR CE	BCL2-RELATED PROTEIN A	INDUCED MYELOID LEUKEM	APOPTOSIS REGULATOR BC	APOPTOSIS REGULATOR BC	APOPTOSIS REGULATOR BC	INSULIN RECEPTOR-RELAT	NODULATION PROTEIN NOL	GLUCAN 1, 3-BETA-GLUCOS	LIGNINASE C PRECURSOR	SIALIDASE PRECURSOR (E	PULLULANASE PRECURSOR	GAG POLYPROTEIN [CONTA	LATENT TRANSFORMING GR	GLUCOSAMINE FRUCTOSE-	NODULATION PROTEIN J.	TRANSALDOLASE (EC 2.2.	TRANSALDOLASE (EC 2.2.	PHOSPHOGLYCERATE KINAS	HYPOTHETICAL 59.4 KD P
BFL1_MOUSE	CED9_CAEBR	BFL1_HUMAN	MCL1_HUMAN	EAR_ASFE4	EAR_ASFM2	EAR_ASFB7	IRR_RAT	NOLO_RHISN	EXG_YARLI	LIGC_TRAVE	NANH_MICVI	PULA_THEMA	GAG_HV2G1	TGFB_RAT	GLMS_THETH	NODJ_BRAJA	TAL1_MOUSE	TAL1_HUMAN	PGKC_LEIME	YBB9_YEAST
4		-	Н	~	Н	-	-	7	П	-	-	-	-	-	-	Н	Н	Ч	٦	Н
172	271	175	350	179	179	179	581	680	421	372	647	843	522	1712	603	262	337	337	479	520
12.0	11.7	11.5	11.5	9.7	9.6	9.6	7.6	7.4	7.1	6.9	6.9	6.9	6.8	6.8	6.7	9.9	9.9	9.9	9.9	9.9
167	162	159	160	134	133	133	105	102	66	95	95	95	94	94	93	92	91	91	91	91
24	26 26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

SUBCELLULAR LOCATION: CYTOLARMIC TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,

AND SALIVARY GLAND.

3888888888888888888888888

-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).

EMBL; U59746; AAB09056.1; -.

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*Journal Cell (1987) 49:455-463
#title Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in #cross-references MUID:87187643
#accession B25960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-199 ##label NEG ##cross-references GB:M16506; NID:9468335; PIDN:AAA37281.1; PID:9387110
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                                                                                                                                                                     Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. (1992) 20:4187-4192
Insolution and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 503; DB 2; Length 206;
Pred. No. 4.22e-76;
30; Mismatches 29; Indels 0; Gaps
                  D37332 *type complete transforming protein (bcl-2-beta) - human *forming protein (bcl-2-beta) - human #formal_name Homo sapiens *common_name man 03.Mar-1993 *sequence_revision 03-Mar-1993 *text_change 23.Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVMSB1 #type complete transforming protein bcl-2-beta - mouse transforming mosculus #common_name house mouse #formal_name Mus musculus #common_name house mouse 31-bec-1988 #sequence_revision 31-bec-1988 #text_change 18-Jun-1999
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mitochondrion
#length 206 #molecular-weight 22440 #checksum 5581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 GVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGW 196
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alternative splicing; transforming protein
#length 199 #molecular-weight 22299 #checksum 7397
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Pred. No. 1.09e-75;
29; Mismatches 31; Indels
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#accession D37332
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Best Local Similarity 48.7%;
Matches 56; Conservative
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Best Local Similarity 48.7%;
Matches 57; Conservative
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Search completed: Fri Jun 23 14:18:26 2000 Job time : 16 secs.

GENETICS #dene KEYWORDS SUMMARY

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1-190 ##label BOI
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Best Local Similarity 5
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#journal Biochim. Biophys. Acta (1992) 1132:109-113
#title Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue of the Bcl-2 oncoprotein.
#cross-references MUID:92379084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 RDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
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#length 236 #molecular-weight 26524 #checksum 6709
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                                                              nucleic acid sequence not shown;
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                                                                                     compared with conceptual translation
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                                                       preliminary;
#cross-references MUID:92375724
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larity 42.8%;
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Best Local Similarity 44.3%;
Matches 70; Conservative
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                                                                                                                            ##molecule_type DNA
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Best Local Similarity
Matches 71; Conserv
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ACCESSIONS ORGANISM DATE

RESULT

REFERENCE

KEYWORDS SUMMARY

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Gaps 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ##cross-references GB:Z23110; GB:L20120; NID:9510898; PIDN:CAA80657.1; PICATION #superfamily bit transforming protein #superfamily bit transforming protein #hength 190 #molecular-weight 21467 #checksum 5509
                                                                                                                                        Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.;
Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 ASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFHDGVNWGRIVA 138
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#title bcl.x, a bcl.2-related gene that functions as a dominant regulator of apoptotic cell death.
#cross-references MUID:93364977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #formal_name Gallus gallus #common_name chicken 03-May-1994 #sequence_revision 03-May-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #formal_name Homo sapiens #common_name man
21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Res. Commun. (1998) 248:147-152 a human cDNA encoding a novel bcl-x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *superfamily bcl transforming protein
#length 227 #molecular-weight 25290 #checksum 864
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Pred. No. 1.09e-82;
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apoptosis regulator bcl-x isoform - human
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Pred. No. 1.09e-82;
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136 RDGVNWGRIVAFFEFGGVMCVGSVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
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#cross-references MUID:87187643
                                                                                                                                                                                                                                                                                                                                                  and T lymphocytes. #cross-references MUID:95052604
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##residues 1-2
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                                                                                                                                                                          immature rat ovary: equine chorion; gene admily in the inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 VANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFATVVEELF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 RDGVNWGRIVAFFEFGGVMCVESVNREMYPLVDNIALWMTEYLNRHLHTWIQDNGGWDAF 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
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BCL-2 - rat (fragment)
#formal_name Rattus norvegicus #common_name Norway rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene bcl-2 protein - rat
#formal_name Rattus norvegicus #common_name Norway rat
29-May-1998 #sequence_revision 29-May-1998 #text_change
16-Jul-1999
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Cloning and sequencing of a CDNA encoding the rat Bcl-2
                                                                                                                                  Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology (1995) 136:232-241
Expression of members of the bcl-2 gene family in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #superfamily bcl transforming protein
#length 236 #molecular-weight 26550 #checksum 8001
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Pred. No. 5.40e-86;
45; Mismatches 43; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 VELYGP-SM---RPLFDFSWQSLKTLLSLAL-VGACITLGAYLGHK 236
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#length 236 #checksum 9134
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Best Local Similarity 43.4%;
Matches 72; Conservative
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Best Local Similarity 42.8%;
Matches 71; Conservative
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Cell (1987) 49:455-463
Molecular analysis of mbcl-2: structure and expression of the
murine gene homologous to the human gene involved in
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Nucleic Acids Res. (1992) 20:4187-4192
Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.
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##cross-references GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1;
PID:g387109
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88 QGGPNWGRLVAFFVFGAALCAESVNREMEPLVGQVQDMIVAYLETRLADMIHSSGGWADF 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. (1994) 153:4388-4398
Cloning and molecular characterization of mouse bcl-x in
and T lymphocytes.
                                                                                                                                                                                                                                            149057 #type complete
bcl-x transmembrane deleted - mouse
#formal_name Mus musculus #common_name house mouse
02.Jul-1996 #sequence_revision 02-Jul-1996 #text_change
16.Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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#formal_name Mus musculus #common_name house mouse
31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bcl-x-long
#superfamily bcl transforming protein
#length 214 #molecular-weight 23900 #checksum 9730
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##cross-references EMBL:U10102; NID:g506649; PIDN:AAA82174.1;
PID:g506650
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Local Similarity 57.9%; Pred. No. 3.92e-84;
les 62; Conservative 24; Mismatches 21; Indels
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                                                                                                                                     148 TALYGDGALEDARRIREGNW-AVSTVVTGAVALGALVTVGAFFASK 192
                                                                                           196 VELYGP-SM---RPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK
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#journal Nucleic Acids Res. (1992) 20:4187-4192
#title Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
#cross-references MUID:92375724
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#title Isolation and characterization of the chicken bcl-2 gene:
expression in a variety of tissues including lymphoid and
neuronal organs in adult and embryo.
#cross-references MUID:92375724
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mitochondrion; transforming protein; transmembrane protein
#length 233 #molecular-weight 25687 #checksum 99
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                                                                                                A37332 #type complete transforming protein (bcl-2-alpha) - chicken #formal_name Gallus gallus #common_name chicken 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
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Proc. Natl. Acad. Sci. U.S.A. (1986) 83:5214-5218
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40.5%; Score 561; DB 2; Length 233;
Best Local Similarity 40.5%; Pred. No. 4.59e-88;
Matches 79; Conservative 47; Mismatches 61; Indels
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161 RLREG-N-WAVSTV-VTGAVALGAL 182
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blocks apoptosis in hematopoietic cells
#superfamily bcl transforming protein
alternative splicing; B-cell lymphoma; follicular lymphoma;
proto-oncogene; transforming protein; transmembrane protein
#length 239 #molecular-weight 26266 #checksum 8323
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Cloning and structural analysis of CDNAs for bcl-2 and a
hybrid bcl-2/immunoglobulin transcript resulting from the t
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##residues 1-58,'T',60-116,'R',118-239 ##label CLE
##cross-references GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
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EMBO J. (1988) 7:123-131
Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2--19 fusion gene in lymphoma.
                               protein products
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#authors Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.;
#yinthors Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.;
#journal Oncogene Res. (1988) 2:263-275
#title Consequences of the t(14;18) chromosomal translocation in follicular lymphoma: deregulated expression of a chimeric and mutated BCL-2 gene.
#cross-references MUID:88217344
#title Analysis of the structure, transcripts, and protein product
    of bcl-2, the gene involved in human follicular lymphoma.
#cross-references MUID:86259760
#accession A29409
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*cross-references MUID:87002488
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Lindsten, T.; Turka, L.A.; Mao, X.; Nunez, G.; Thompson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 VFGAALCAESVNKEMEPLVGQVQDMIVAYLETRLADMIHSSGGWADFTALYGDGALEDAR 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #journal Cell (1993) 74:597-608
#title bcl.x, a bcl.2-related gene that functions as a dominant
regulator apoptotic cell death.
#cross-references MUD:93364977
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apoptosis regulator bcl-xL - human
bcl-2-related protein
apoptosis regulator bcl-xs
#formal_name Homo sapiens #common_name man
16.4wg-1996 #sequence_revision 16-Aug-1996 #text_change
                                  BCL-X protein rat #formal_name Norway rat 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 16-Jul-1999
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#superfamily bcl transforming protein
#length 233 #molecular-weight 26130 #checksum 6378
                                                                                                                                                                                                                       ##residues
##cross-references EMBL:X82537; NID:g607176; PIDN:CAA57886.1;
PID:g607177
                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-125,189-233 ##label MI2
##cross-references EMBL:X82537; NID:g607176; PIDN:CAA57887.1;
PID:g607178
                                                                                                                                       Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994
S51761
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Pred. No. 5.74e-101;
34; Mismatches 32;
                    #type complete
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Best Local Similarity 52.4%;
Matches 76; Conservative
                                                                                                      S51761; S51762
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                                                                                                                                                                                                            ##molecule_type_DNA
##residues 1-2
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##cross-references GB:L20121; NID:g510900; PIDN:CAA80661.1; PID:g510901

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#authors Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
#journal Endocrinology (1995) 136:232-241
#title Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
                                                                                                 ##residues 1-69,'G',71-125,189-233 ##label BO2
##cross-references GB:L20122; NID:9623236; PIDN:CAA80662.1; PID:9623237
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                                                                                                                                                                                                                                                                                                                                                                     #product apoptosis regulator bcl-xS #status predicted
#label MA2
#length 233 #molecular-weight 26063 #checksum 5340
                                                                                                                                                                                                                                                                                                                      #product apoptosis regulator bcl-xL #status predicted
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#formal_name Rattus norvegicus #common_name Norway rat
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
16-Jul-1999
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#length 233 #molecular-weight 26122 #checksum 8310
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##molecule_type mRNA
##residues 1-233 ##label RES
##cross-references EMBL:034963; NID:91004376; PIDN:AAA77686.1;
##cross-references PID:91004377
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161 RLREG-N-WAVSTV-VTGAVALGAL 182
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                                                     GB/EMBL/DDBJ
                                                                                                                                                                                                              ##cross-references GDB:228079
                                                                                                                                                                                                                                                                                                                                                  #label MAT\
                                                                              ##molecule_type mRNA
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protein - protein database search, using Smith-Waterman algorithm Fri Jun 23 14:18:10 2000; MasPar time 12.63 Seconds 716.856 Million cell updates/sec MPsrch_pp

Tabular output not generated.

Description: Perfect Score: Sequence:

>US-09-155-327B-9
(1-192) from US09155327B.pep
1386
1 MPTPASTPDTRALVADFVGY......VTGAVALGALVTVGAFFASK 192

PAM 150 Gap 11 Scoring table:

142080 seqs, 47172406 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Mean 44.905; Variance 86.927; scale 0.517 Statistics:

pir63 1:pir1 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 623 44.9 233 2 149056 bcl-x long - mouse 5.74e- 2 623 44.9 233 2 551761 BcL-x protein - rat 5.74e- 3 624 22 233 2 551761 apoptosis rat 5.74e- 4 585 42.2 233 2 167431 BCL-X-Long - rat 6.78e- 5 561 40.5 233 2 167431 ECL-X-Long - rat 6.78e- 6 556 40.1 239 1 TVHUAL	Result No.	Score	& Query Match	å Query Match Length DB	6	ΩI	Description	Pred. No.
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542 39.1 236 1 TVMSA1 transforming protein 540 39.0 232 2 S24390 transforming protein 535 38.6 130 2 A77537 apoptosis regulator b 535 38.6 227 2 JE0203 transforming protein 501 36.1 199 1 TVMSB1 transforming protein 495 35.7 2 16 2 B37332 transforming protein 491 35.4 205 1 TVMUB1 transforming protein 491 35.4 205 1 TVMUB1 transforming protein 401 29.1 154 258873 apoptosis. Totolin - 235 17.0 211 2 S58873 apoptosis human 234 16.9 211 2 S58873 bcl2-associated prot 226 16.3 192 2 A47538 bcl2-associated prot	6	542	39.1	214	~	I49057	bcl-x transmembrane d	3.92e-84
540 39.0 232 2 524390 transforming protein 535 38.6 190 2 A47537 apoptosis regulator b 535 38.6 190 2 A47537 apoptosis regulator b 503 36.3 206 2 D37332 transforming protein 404 25.1 199 1 TVMUBB1 transforming protein 495 35.7 206 1 TVMUBB transforming protein 404 29.1 154 2 158194 gene bc.1-2 protein - 235 17.0 211 2 558873 Bak protein - 234 16.9 211 2 558873 Bak protein - human 234 16.9 2 11 2 558875 bc.1-2 protein - human 235 16.8 192 2 A47538 bc.1-2-associated protein 26.3 16.3 192 2 A47538 bc.1-2-associated protein 26.3 192 2 A47538 192 2	0	542	39.1	236	Н	TVMSA1	transforming protein	3.92e-84
535 38.6 190 2 A47537 apoptosis regulator b 503 38.6 227 2 JBD203 apoptosis regulator b 503 36.3 206 2 JBD203 apoptosis regulator b 503 36.3 206 2 JBD332 transforming protein 495 35.7 216 2 B37332 transforming protein 491 35.4 205 1 TVHUB1 transforming protein 404 29.1 154 2 158194 gene bcl-2 protein - 235 17.0 211 2 558873 Bak protein - human 234 16.9 2 11 2 558875 cdn-2 protein - human 233 16.8 192 2 D47538 bcl-2-associated prot 26 16.3 193 2 A47538 bcl-2-associated prot 26 16.3 193 2 A47538 bcl-2-associated prot 26 16.3 192 2 A47538 bcl-2-associated prot 26 16.3 192 2 A47538 bcl-2-associated prot 26 16.3 192 2 A47538 bcl-2-associated prot	_	540	39.0	232	7	S24390	transforming protein	1.01e-83
535 38.6 227 2 JE0203 apoptosis regulator b 503 36.3 206 2 D373.2 transforming protein 501 36.1 199 1 TVWASB1 transforming protein 495 35.7 216 2 B37332 transforming protein 491 35.4 205 1 TVWUB1 transforming protein 491 35.4 205 1 TVWUB1 transforming protein 235 17.0 2 11 2 558873 Bak protein - 234 16.9 211 2 558873 Bak protein - human 234 16.9 211 2 558875 cdn-2 protein - human 235 16.8 192 2 D47538 bcl-2-associated prot 26 16.3 192 2 A47538 bcl-2-associated prot 26 16.3 192 2 A47538 bcl-2-associated prot	~	535	38.6	190	7	A47537	apoptosis regulator b	1.09e-82
503 36.3 206 2 D37332 transforming protein 495 35.7 1 199 1 TVMSB1 transforming protein 495 35.7 2 16 2 B3732 transforming protein 491 35.4 205 1 TVHUB1 transforming protein 404 29.1 154 2 159194 gene bc.1-2 protein - 235 17.0 211 2 558873 Bak protein - human 234 16.9 2 11 2 558875 cdn-2 protein - human 233 16.8 192 2 D47538 bc.1-2-associated prot 226 16.3 192 2 A47538 bc.1-2-2-associated prot 226 16.3 16.3 16.3 16.3 16.3 16.3 16.3 16.	m	535	38.6	227	~	JE0203	apoptosis regulator b	1.09e-82
501 36.1 199 1 TVMSB1 transforming protein 495 35.7 216 2 B3732 transforming protein 491 35.4 205 1 TVHUB1 transforming protein 404 29.1 154 2 158194 gene bcl-2 protein - 235 17.0 211 2 558873 Bak protein - 1 LL 258875 cdn-2 p	4	503	36.3	206	~	D37332	transforming protein	4.22e-76
495 35.7 216 2 B37332 transforming protein 491 35.4 205 1 TWHUBB transforming protein 404 29.1 154 2 158194 gene bcl.2 protein - 235 17.0 211 2 558873 Bak protein - human 234 16.9 211 2 558875 cdn.2 protein - human 231 16.8 192 2 D47538 bcl.2-associated prot 226 16.3 192 2 A47538 bcl.2-associated prot 226 16.3 192 2 A47538 bcl.2-associated prot	S	501	36.1	199	-	TVMSB1	transforming protein	1.09e-75
491 35.4 205 1 TVHUB1 transforming protein 401 29.1 154 2 158194 gene bcl-2 protein - 235 17.0 211 2 558873 Bak protein - human 234 16.9 211 2 558875 cdn-2 protein - human 233 16.8 192 2 D47538 bcl-2-associated prot 226 16.3 143 2 1318921 bcl-2-associated prot 226 16.3 192 2 A47538 bcl-2-associated prot 226 18.3 192 2 A47538 bcl-2-associated prot 226 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	٥	495	35.7	216	7	B37332		1.85e-74
404 29.1 154 2 158194 gene bcl-2 protein - 235 17.0 211 2 558873 Bak protein - 14.0 213 2 558875 cdn-2 protein - 14.0 213 16.9 2 2 11 2 558875 cdn-2 protein - 14.0 213 16.9 2 2 11 2 528921 bcl-2-associated prot 226 16.3 143 2 138921 bcl-2-associated prot 26 16.3 192 2 447538 bcl-2-associated prot 226 16.3 192 2 447538	7	491	35.4	205	٦	TVHUB1		1.22e-73
235 17.0 211 2 558873 Bak protein - human 234 16.9 211 2 558875 cdn-2 protein - human 234 16.8 192 2 047538 bcl-2-associated prot 226 16.3 192 2 447538 bcl-2-associated prot 226 16.3 192 2 447538 bcl-2-associated prot	æ	404	29.1	154	7	158194	gene bcl-2 protein -	5.41e-56
234 16.9 211 2 558875 cdn-2 protein - human 23 16.8 192 2 D47538 bcl-2-associated prot 226 16.3 143 2 138921 bcl-2-associated prot 226 16.3 192 2 A47538 bcl-2-associated prot	6	235	17.0	211	7	S58873	•	2.90e-23
233 16.8 192 2 D47538 bcl-2-associated prot 226 16.3 143 2 138921 bcl-2-associated prot 226 16.3 192 2 A47538 bcl-2-associated prot	0	234	16.9	211	7	S58875	protein -	4.43e-23
226 16.3 143 2 138921 bcl-2-associated prot 1 226 16.3 192 2 A47538 bcl-2-associated prot 1	_	233	16.8	192	7	D47538		9
16.3 192 2 A47538 bcl-2-associated prot 1	ď	226	16.3	143	N	138921		1.29e-21
	m	226	16.3	192	~	A47538		1.29e-21

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205 KGQERFNRWFLTGMTVAGVVLLGSL 229 ::| | | | :: : |:| | | |:|

1.96e-21 1.26e-19 7.78e-18	3.99e-17 4.55e-16 2.92e-11	6.31e-11 6.23e-10 4.27e-10	1.84e-01 4.58e-01 1.12e+00	1.12e+00 2.01e+00 2.01e+00	2.01e+00 2.69e+00 2.69e+00	2.69e+00 2.69e+00 3.58e+00
bcl-2-associated prot bcl-2-associated prot bcl-x short - mouse	gene bcl-xshort prote NR-13 protein - quail hemopoietic-specific	apoptosis suppressor Bcl-2 related - human BCL2 homolog MCL1 - h	hypothetical protein angiotensin-convertin probable transitional	probable polyketide s lignin peroxidase (EC exo-alpha-sialidase (pullulanase - Thermot hypothetical protein gag polyprotein - hum	masking protein precu fatty-acid synthase (hypothetical protein
153295 B47538 149055	167435 S54778 149449	A53189 I39055 A47476	T03168 JC5374 B71196	T03224 S32581 A45244	H72204 C70667 FOLJGG	A38261 S20473 E70529
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ALIGNMENTS

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    Query Match
Best Local Similarity 22.7%; Pred. No. 1.23e-12;
Matches 30; Conservative 31; Mismatches 70; Indels 1; Gaps 1;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MYELOID CELL LEUKEMIA PROTEIN MCL-1 (FRAGMENT).
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 -PNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 PGRASSAVMEKALETLRRVGDGVMQKHELAFQGMLRKLEIKKEDDLQAVCEVAAQVFNDG 114
                                                                                                                                                                                                     72 PGSAQQRFTQVSDELFQGG-PNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDMIVAXL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 VTNWGRVVTLISFGAFVAKHLKSINQEKCITSLAGIITDALVSSKREWLMSQGGWEGFVD 174
                                                                                                                                    160 EIISRY-LREQATGSKDAKPLGEAGAAGRRALETLRRVGDGVQRNHETAFQGMLRKLDIK 218
                                                                                                                                                                                       219 NEDDVKSFSRVMTHVFKDGVTNWGRIVTLISFGAFVAKHLKSINQESCIEPLAESITDVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
MEDLINE; 99190706.
LEE R.M., GILLET G., BURNSIDE J., THOMAS S.J., NEIMAN P.:
"Role of Nr13 in regulation of programmed cell death in the bursa of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 AGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQORFTQVSDELFQGG 90
                                                                                                                                                    16 DFVG-YRLRQKGYVC-GAGP-GE-GPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVT 71
                                                                                                            Gaps
                                                                                                           9
                                                                               / Match 12.6%; Score 175; DB 11; Length 330; Local Similarity 24.5%; Pred. No. 6.35e-14; hes 37; Conservative 33; Mismatches 75; Indels
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF115380; AAD13295.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFER L., BURNSIDE J.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF120210; AAD31644.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
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                           HSSF, Q07817; IMAZ.
PROSITE; PS01080; BH1; 1.
SEQUENCE 330 AA; 35195 WW; CC87F2E0 CRC32;
                                                                                                                                                                                                                                                                                                                          211 AA
                                                                                                                                                                                                                                            279 VRTKRDWLVKQRGWDGFVEFFHVQDLEGGIR 309
                                                                                                                                                                                                                                                             131 ETRLADWIHSSGGWADFTALYGDGALEDARR 161
                                                                                                                                                                                                                                                                                                                          PRT;
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O77738;
O1-NOV-1998 (TrEMBLrel. 08, Cr
O1-NOV-1999 (TrEMBLrel. 08, La
O1-NOV-1999 (TrEMBLrel. 12, La
BAK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes Dev. 13:718-728(1999)
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                                                                                   Query Match
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Q9W6F1
Q9W6F1;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NUV-1999 (TrEMBLrel. 12, Last annotation update)
B-CELL LERKEMIA/LYMPHOMA 2 RELATED PROTEIN ALC (Al-C PROTEIN).
BCL2AIC OR ALC.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-129/SV; TISSUE-LIVER;
HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,
NAKAYAMA K., NAKAYAWA K.-I.;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 144; DB 6; Length 80;
Pred. No. 2.28e-08;
15; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 GDDINRRYDSEFQAMLQHLQPTAENAYEYFTKIASSLFESGINWGRVV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myocardium of pig.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ001204; CAA04598.1; -.
HSSP; Q16611; 1BXL.
PROSITE; PG01259; BH3; 1.
PROSITE; PG01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 DFHVESIDTTRIIFNQVMEKEFEDGIINWGRIVTIFAFGGVL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 120; DB 11;
Pred. No. 2.21e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1278327; Bcl2alc.
PROSITE; PS01080; BHL; 1.
PFAM: PF00452; Bcl-2: 1.
SEQUENCE 128 AA; 14763 MW; DF4F2653 CRC32;
                                                                                                                                                                                                                                                                                                                                                                       80 AA; 8818 MW; 973BE2D0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Int. Immunol. 0:0-0(1998).
EMBL; U23779; AAB97955.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.7%;
Best Local Similarity 38.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 35.4%;
Matches 17; Conservative
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                                                                                              SEQUENCE FROM N.A.
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NON_TER
SEQUENCE
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055178
055178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 SPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASPAPGG-RLAEVCTVLLRLGITWG 79
                                                                                                                                                   Gaps
                                                                                                     'n
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                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
B-CELL LEUXEMIA/LYMPHOMA 2 RELATED PROTEIN AlB (Al-B PROTEIN).
                                                                                                                                                                                                                 80 KVVSLYSVAAGLAVDCVRQAQPAMVHALVDCLGEFVRKTLATWLRRRGGWTD 131
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
B-CELL LEDKEMIA/LYMPHOMA 2 RELATED PROTEIN AID (A1-D PROTEIN)
BCL2AID OR AID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                 Ouery Match 12.7%; Score 176; DB 11; Length 170; Best Local Similarity 25.0%; Pred. No. 4.14e-14; Matches 28; Conservative 35; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-129/SV; TISSUE-LIVER;
HATAKEYAMA S., HAMASAKI A., NEGISHI I., LOH D.Y., SENDO F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 172;
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STRAIN-129/SV; TISSUE-LIVER;
HATAKEVAMA S., HAMASKAI A., NEGISHI I., LOH D.Y., SENDO F.,
NAKAYAMA K., NAKAYAMA K.-I.;
Int. Immunol. 0:0-0(1998).
EMBL; U23781; AAB97956.1; -.
EMBL; U23780; AAB97956.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF051093; AAC61928.1; ·. SEQUENCE 170 AA; 18729 MW; 79B4BBE6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 6.35e-14;
20; Mismatches 30;
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SEQUENCE 172 AA; 20048 MW; FA16DF6C CRC32;
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Local Similarity 33.7%; Pred. No. 6
nes 29; Conservative 20; Mismat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAKAYAMA K., NAKAYAMA K.-I.;
Int. Immunol. 0:0-0(1998).
EMBL; U23778; AAB97954.1; --
EMBL; U23777; AAB97954.1; --
MGD; MGI:1278326; BG12alb.
PROSITE; PS01080; BH1; 1.
                                                                                                                                                                                                                                                                                                PRELIMINARY;
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055177
055177;
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055179
055179;
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Gallus gallus (Chicken)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                 58 DFHVESIDTARIIFNQVMEKEFEDGIINWGRIVTIFAFGGVL-LKKLPQEQIALDVGAYK 116
                                                                                                                                                     87 GRIMTIFTFGGLL-TKKLQEHGVQLTGEEKEKISYFITEYIINNKAAWIDANGGWENGFL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 99190706.
LEE R.M., GILLET G., BURNSIDE J., THOMAS S.J., NEIMAN P.;
"Role of Nr13 in regulation of programmed cell death in the bursa of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.6%; Score 174; DB 13; Length 174;
Best Local Similarity 24.4%; Pred. No. 9.71e-14;
Matches 30; Conservative 33; Mismatches 52; Indels 8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 GPAQTRVAHVLRNIASSLQDQTEEALRPFLDRIDITSVDVAKRIFNGVMEEKFADGNTNW 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                             Length 172;
                                                                        Score 174; DB 11; Length 172, Pred. No. 9.71e-14; 20; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFER L., BURNSIDE J.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF120211; AAD31645.1; -.
SEQUENCE 174 AA; 20095 MW; 70F5FDAA CRC32;
                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
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SEQUENCE FROM N.A.
LEO C.P., HSU S.Y., HSUEH A.J.W.;
"Sequence of rat Mcl-1, a Bcl-2-related gene.";
MGD; MGI:1278325; Bcl2ald.
PROSITE; PS01080; BH1; 1.
PRAM; PPC0452; Bcl-2; 1.
SEQUENCE 172 AA; 20048 MW; 1B340DDD CRC32;
                                                                                                                                                                                                                                                                                        174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 AA
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-NOV-1999 (TrEMBLrel. 12, Last ann
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01-MAY-1999 (TrEMBLrel. 10, Last sequ
01-NOV-1999 (TrEMBLrel. 12, Last anno
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                                                                                                                                                                                            117 OVSSFVAEFIMNNTGEWIRRNGGWED 142
                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes Dev. 13:718-728(1999).
                                                                        Query Match 12.6%;
Best Local Similarity 33.7%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                      PRELIMINARY;
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SEQUENCE FROM N.A.
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09W6F2
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Q9Z1P3
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"Bok is a pro-apoptotic Bcl-2 protein with restricted expression in reproductive tissues and heterodimerizes with selective anti-apoptotic Bcl-2 family members.";

Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIANA N., EKHTERAE D., GARCIA I., CARRIO R., MERINO J., MERRY A., CHEN S., NUNEZ G.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF0277954; AAAB97418.1; -.
EMBL; AF0277707; AAC53582.1; -.
PFAM; PF00452; Bc1-2: 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                     Length 170;
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                                                                                                                                                                                                                                                                                                                                          85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQDSFVDLY 132
                                                                                                                                                                                                                                                                                                                                                                          HE X.J., JIN K.L., GRAHAM S.H., SIMON R.P.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF136230; AAD33683.1; -.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4.1; 1.
SEQUENCE 170 AA; 19031 MW; 8B29C9C1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSU S.Y., HSUEH A.J.W.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, UTERUS; MEDLINE; 98024143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 05, Last sequence update) (TrEMBLrel. 08, Last annotation update)
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                                                                                                                                                                                                                  Score 207; DB 11;
Pred. No. 5.41e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23456 MW; 29761D17 CRC32;
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                                                                                                                                                                                                                                                                                 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 213 AA
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                                                                                                                                                                                                                     / Match 14.9%;
Local Similarity 58.3%;
hes 28; Conservative
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Matches 28; Conservative
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P97287;
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Last sequence update)
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HSU S.Y., KAIPIA A., MCGEE E., LOMELI M., HSUEH A.J.; "Bok is a pro-apoptotic Bcl-2 protein with restricted expression in reproductive tissues and heterodimerizes with selective anti-apoptotic Bcl-2 family members.";
                                                                                                                                                                                                                                                                    CHAO J.R., WANG J.M., IEE S.F., PENG H.W., LIN Y.H., CHOU C.H.,
LI J.C., HUDANG H.M., CHOU C.K., KUO M.L., YEN J.J.Y., YANG-YEN H.F.;
"mcl-1 is an immediate-early gene activated by the granulocyte-
macrophage colony-stimulating factor (GM-CSF) signaling pathway and is
one component of the GM-CSF viability response.";
Mol. Cell. Biol. 18:4883-4898(1998).
ENBL; AD5623; AAC31790.1; -.
ENBL; ARC53886; AAC37929.1; -.
HSSP; Q07817; IMAZ.
MGD; MGI:101769; Mcl1.
PROSITE; PS01080; BHl. 1.
FROM; PFO452; BCl-2; 1.
SEQUENCE 331 AA; 35217 MW; 3103C5FE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-OVARY, UTERUS;
HSU S.Y., HSUEH A.J.W.
"A splicing variant of the Bcl-2 member Bok with a truncated BH3
domain induces apoptosis without dimerization with anti-apoptotic Bcl-
                                                                                                        OKITA H., UMEZAMA A., SUZUKI A., HATA J.;

"Up-regulated expression of murine Mcll/EAT, a bcl-2 related gene, in the early stage of differentiation of murine embryonal carcinoma cells and embryonic stem cells."

Biochim. Biophys. Acta 1398:335-341(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 NWGRIVTLISFGA-FVAKHLKSVNQESFIEPLAETITDVLVRTKRDWLVKQRGWDGFVEF 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 NWGRLVAFFVFGAALCAESVNK-EMEPLVGQVQDMIVAYLETRLADWIHSSGGWADFTAL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GEAGAAGRRALETLRRVGDGVQRNHETAFQGMLRKLDIKNEGDVKSFSRVMVHVFKDGVT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 GE-GPAADPLHQAMRAAGDEFETRFRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGG-P 91
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 177; DB 11; Length 331; Pred. No. 2.70e-14;
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
BCL-2-RELATED OVARIAN KILLER PROTEIN.
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nes 33; Conservative
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TISSUE=OVARY, UTERUS;
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                                                                                                                                                                                                                                                              MEDLINE; 98336293.
                                                                             SEQUENCE FROM N.A. MEDLINE; 98322120.
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229 AA; 25099 MW; E82B3DFB CRC32;

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035843;
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Q9WUI5
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                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                        YANG X.-F., WEBER G.F., CANTOR H.;
"A novel Bcl-x isoform connected to the T cell receptor regulates apoptosis in T cells.";
Immunity 7:629-639(1997).
EMBL; 051278; AAC53459.1; -.
HSSP; P53563; lAF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovíne).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                     .
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                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                  Score 638; DB 11; Length 233;
Pred. No. 2.64e-113;
34; Mismatches 31; Indels
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                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                            MGD; MGI:88139; BG121.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01259; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
PROMIP: PS00452; BG1-2; 1.
SEQUENCE 233 AA; 26033 WW; A4A14278 CRC32;
                                 233 AA
                                  PRT;
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161 RLREG-N-WAVSTV-VTGAVALGAL 182
                                                                                                                         [1]
SEQUENCE FROM N.A.
STRAIN-B6/CBA; TISSUE-THYMUS;
MEDLINE; 98051053.
                                                 (TrEMBLrel. 05, (TrEMBLrel. 05, 1 (TrEMBLrel. 12, 1
                                                                                                                                                                                                                                                                                  y Match 46.0%;
Local Similarity 53.1%;
hes 77; Conservative
                                  PRELIMINARY;
180 GALVTVGAFFASK 192
                                                                            BCL2-LIKE (BCL-XL).
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                                                  01-JAN-1998
01-JAN-1998
                                                                    01-NOV-1999
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035844;
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N MEDLINE; 9061053.

YANG X.-F., WEBER G.F., CANTOR H.;

"A novel Bcl-x isoform connected to the T cell receptor regulates
T apoptoosis in T cells.";

Immunity 7:629-639(1997).

R HSSP; 5736; JAR3.

R HSSP; S1363; JAR3.

R RSSP; S1363; JAR3.

R PROSITE; PS01080; BH1; 1.

R PROSITE; PS01269; BH4_1; 1.

R PROSITE; PS01260; BH4_1; 1.
                                                                                                                71 AAGPAPSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARERFATVVEELFRD 130
                                                                                                                                                                                                                                                           85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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                                                                                                                                             :|||: :| : :| ::| |||: | ||:|| 30 GAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQG 89
                                                            6; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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        Length 229;
Score 560; DB 6; Length 229,
Pred. No. 1.15e-95;
48; Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                                   ||| ::. | |: :| ::: | |: || || 150 LYGDGALEDARRLREGNW-AVSTVVTGAVALGALVTVGAFFASK 192
                                                                                                                                                                                                                                                                                                                                         191 LYGP-SM---RPLFDFSWLSLKALLSLAL-VGACITLGAYLGHK 229
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Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequ
01-NOV-1999 (TrEMBLrel. 12, Last anno
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     Match 40.4%;
Local Similarity 42.7%;
Les 70; Conservative
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Best Local Similarity 58.1%;
Matches 61; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Fri Jun 23 14:19:13 2000; MasPar time 19.74 Seconds 674.404 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-155-327B-9 (1-192) from US09155327B.pep 1386

1 MPTPASTPDTRALVADFVGY......VTGAVALGALVTVGAFFASK 192 Title: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

225878 segs, 69334122 residues

sptremb112 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 5:sp_hade 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 44.372; Variance 79.166; scale 0.560 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2. 256-277 2. 64e-113 3. 25e-277 3. 1.62e-89 3. 1.66-15 4. 14e-14 4. 14e-14 6. 35e-14 6. 35e-14 7. 16-14 7. 16-14 7. 16-14 8. 57e-04 8. 67e-02 8. 67e-02	
P.		
Description	BCL-W. BCL2-LIKE (BCL-XL). BCL2-LIKE (BCL-XL). BCL2-LIKE (BCL-X-GAMMA BCL2-LIKE (BCL-X-GAMMA BCL-X-RELATED OVARIAN EAT/ACL-1 PROTEIN (MCL-2-RELATED OVARIAN B-CELL LEUKEMIA/LYMPHO B-CELL LEUKEMIA/LYMPHO B-CELL LEUKEMIA/LYMPHO BCLI LEUKEMIA/LYMPHO BCLI LEUKEMIA/LYMPHO BCLL LEUKEMIA/LYMPHO WCLEAR TRANSPORT RECE SIMILAR TO BCL-FAMILY GAG PROTEIN (FRAGMEWT) B-CELL LEUKEMIA/LYMPHO WCLEAR TRANSPORT RECE SIMILAR TO BCL-FAMILY GAG PROTEIN (AZCL-1 4 PROTEIN (AZCL-1 4 PROTEIN)	
ID	088996 035844 0035844 0035844 0035848 035843 0055177 0055177 00986F2 00986F2 00986F2 00986F2 00986F3 00986F3 00986F3 00986F3 00987F1	
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Score	1343 638 538 539 1075 1176 1176 1177 1170 1170 1170 1170 1170	
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3.25e-01 4.50e-01 6.22e-01 6.22e-01 6.22e-01 6.22e-01 1.62e+00 1.62e+00 1.62e+00 1.62e+00	1.62e+00 2.21e+00 2.21e+00 2.21e+00 4.10e+00 4.10e+00 4.10e+00 4.10e+00
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P90504 Q9WRT6 Q9Y5L0 Q92657 Q9YUR4 G59518 Q18965 Q18965 G7148 Q51585 Q51585 Q51585 Q51585 Q51585	004846 092312 097513 097625 007192 P70703 000751 027209 030061
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                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: BCI-x*/BCI-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
                                                                                                                                                                                                                                                                                Ouery Match
44.9%; Score 623; DB 1; Length 233; Best Local Similarity 52.4%; Pred. No. 7.82e-45; Matches 76; Conservative 34; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
STREET: 379 Lytton Avenue
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
AURIENT APPLICATION DATA:
AUBLICATION NUMBER: US/08/081,448
FILING DATE: 19930622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 AA
                                                         APPLICATION NUMBER: US/08/661,479 FILING DATE: 11-UW-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE 233 AA; 26063 MW; 275311 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 59, Application US/08661479 Patent No. 5834209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 59, Application US/08661479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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RLREG-N-WAVSTV-VTGAVALGAL 182
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STATE: California
COUNTRY: US
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US-08-661-479-59
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CC APPLICATION NUMBER: US 08/333,565
CC ATTORNEY/AGENT INFORMATION:
CC ATTORNEY/AGENT INFORMATION:
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 15726A-000700
CC TELECOMMUNICATION INFORMATION:
CC TELECOMMUNICATION INFORMATION:
CC TELEFAX: (415) 326-2402
CC TELEFAX: (415) 326-2402
CC TELEFAX: (415) 326-2402
CC TENETH: 233 amino acids
CC TENETH: 234 amino aci
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Search completed: Fri Jun 23 14:20:05 2000 Job time: 9 secs.

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Chicago
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US-08-081-448-6
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TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                           ä
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                                                                                                                                                                                                                                                                                                                                                                                            3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 59, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: BC1-x/Bc1-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                       Score 623; DB 3; Length 233; Pred. No. 7.82e-45; 34; Mismatches 32; Indels
                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 AA.
                                                                                                                                                                                                                                                  23647-20007.20
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                                                                                                                                                                                                                                                                                                                                                      233 AA; 26049 MW; 275801 CN;
                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-007-1994
ATTORNEY/AGENT INFORMATION:
                             NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORRSTER
STREET: 755 Page Will Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 59, Application US/08333565
                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,943
REGISTRATION NUMBER: 33,943
RELECOMMULCATION INFORMATION:
TELEPHONE: (415) 813-5600
TELERX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 14:
                                                                                  COMPUTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATABLE
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161 RLREG-N-WAVSTV-VTGAVALGAL 182
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                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
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Local Similarity 52.4%;
Les 76; Conservative
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                                                                 CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                           FILING DATE:
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US-08-333-565-59
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 623; DB 1; Length 233;
Pred. No. 7.82e-45;
34; Mismatches 32; Indels 3; Gaps
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Arnold, White & Durkee
321 No. 5646008th Clark Street, Suite 800
                                                                                                                                                     COMPUTER, READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FO Compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08081448
Patent No. 5646008
GENERAL INFORMATION
APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          15726A-000700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: peptide
JENCE 233 AA; 26049 MW; 275801 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Smith, William M
REGISTATION UNDRER: 30,223
REFERENCE/DOCKET UNDRER: 15726
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08081448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Best Local Similarity 52.4%;
Matches 76; Conservative
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 623; DB 4; Length 233; Pred. No. 7.82e-45; 34; Mismatches 32; Indels
                                                                                          TITLE OF INVENTION: Vertebrate Apoptosis Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 AA.
233 AA
                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/081.448
FILING DATE: 22 JUNE 1993
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, David L.
REGISTRATION NUMBER: 32,165
REFRENCE/DOCKET UNMBER: ARCD090
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US94/07089 FILING DATE: CONCURRENTLY FILED
                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                            United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
PRT;
                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
TRNCE 233 AA; 26049 MW; 275801 CN;
                                                                 Sequence 7, Application PC/TUS9407089 GENERAL INFORMATION:
                                                 Sequence 7, Application PC/TUS9407089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08470670A
                                                                                                                                                                                                                                                                                                                    TELEFAX: 713-789-20/>
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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TELEPHONE: 512-22
TELEPHONE: 713-789-2679
                                                                                                                                                                             COMPUTER READABLE FORM:
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Best Local Similarity 52.4%;
Matches 76; Conservative
                                                                                                  TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                           CITY: Houston
                                                                                                                                                           COUNTRY: Un
PCT-US94-07089-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-470-670A-7
                                                                                  APPLICANT:
                                                                                                                                                    STATE:
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85 AVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFF 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
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                                                                                                                                                                                                                                                                                                         STATE: Texas
COUNTR: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DARE:
APPLICATION NUMBER: US/08/470,670A
                                                                  GENERAL INFORMATION:
APPLICANT: Thompson, Craig B. B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. BOX 4433
CITY: Houston
STATE: Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/081,448 FILING DATE: 22-JUN-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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JENCE 233 AA; 26063 MW; 275311 CN;
Sequence 7, Application US/08470670A Patent No. 5834309
Patent No. 5834309 5710045
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Patent No. 6015687
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: 'Highlander, Steven L.
REGISTRATION INDRBER: 37,642
REFERENCE/DOCKET UNDBER: ARCD
TELECOMMUNICATION INFORMATION:
TELEFONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08471057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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Matches 76; Conservative
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121 VQEWMYAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180

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        1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 192;
                                                                                                                                                                                                                                                     ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                Sequence 6, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICART: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/798,897 FILING DATE: February 11, 1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.7%; Score 1326; DB 1; I
Best Local Similarity 94.3%; Pred. No. 2.75e-109;
Matches 181; Conservative 8; Mismatches 2;
                                                                                                                    192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        1483.0140001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LE TYPE: protein
192 AA; 20701 MW; 181510 CN;
                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ESEMOM, RODERT 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2500
TELEPHONE: 202-371-2500
                                                                                                                                                                     Sequence 6, Application US/08798897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: not relevant TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                      Washington
                                                                   181 ALVTVGAFFASK 192
                                                                            181 ALVTVGAFFASK 192
                                                                                                                                                                                                                                                                                       USA
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145 SFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESR 204
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Pred. No. 7.82e-45;
34; Mismatches 32; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                   Sequence 24, Application PC/TUS9504600
GENERAL INFORMATION:
APPLICANT: LA JOLIA CANCER RESEARCH FOUNDATION
TITLE OF INVENTION: Interaction of Proteins Involved in
TITLE OF INVENTION: a Cell Death Pathway
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                       233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: FP-LJ 1361
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US95/04600 FILING DATE: 12-APR-1995 CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: Imbra, Richard J. REGISTRATION NUMBER: 37,643
                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
HCE 233 AA; 26063 MW; 275311 CN;
                                                                                                                                                                                                                                                                                                              Sequence 24, Application PC/TUS9504600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 KGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 52.4%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Diego
STATE: California
                                                              181 ALVTVGAFFASK 192
                                                                                      181 ALVTVGAFFASK 192
                                                                                                                                                                                       PCT-US95-04600-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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192 amino acids
                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202-371-2540
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                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.7%;
Best Local Similarity 94.3%;
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                  CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                       181 ALVTVGAFFASK 192
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                                      SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 120
                                                                           121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 180
                                                                                      62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
1 ATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRTF 60
          2 PTPASTPDFRALVADEVGYRLRQKGYVCGAGPGEGPAADPLEQAMRAAGDEFETRFRRTF 61
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                                                                                                                                                                                                                                                                                                                 AUDICESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 192;
                                                                                                                                                                                                                                                      Sequence 5, Application US/08798897
Patent No. 5782201
GENERAL INFORMATION:
APPLICART Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
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Pred. No. 7.67e-110;
7; Mismatches 1;
                                                                                                                                                                            192 AA
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HENCE 192 AA; 20689 MW; 183185 CN;
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TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 aming acids
                                                                                                                                                                                                                                     Sequence 5, Application US/08798897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not relevant
                                                                                                                                                                            STANDARD;
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Local Similarity 95.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                   181 ALVTVGAFFASK 192
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                           62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF SEQUENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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Pred. No. 2.75e-109;
                                                                                                                                                                                                                                                                                                                                                                          192 AA.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BSmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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JENCE 192 AA; 20701 MW; 181510 CN;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                           121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                               FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
          MATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
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Pred. No. 2.65e-110;
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STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                 Sequence 4, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICART: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: FEBRUARY 11, 1997
CLASSIFICATION: 424
                                                                                                                                                             193 AA
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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MOLECULE TYPE: protein
FENCE 193 AA; 20832 MW; 183365 CN;
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                                                                                                                                                                                                                  Sequence 4, Application US/08978523
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LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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TELEPHONE: ZUZ ...
202-371-2540
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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Best Local Similarity 94.3%;
Matches 182; Conservative
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Pred. No. 7.67e-110;
7; Mismatches 1; Indels
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Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: 6 FOR PCL-2
STREED: STRRE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STRRET: Washington
CITY: Washington
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: FEBRUARY 11, 1997
CLASSIFICATION: 424
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FENCE 192 AA; 20689 MW; 183185 CN;
                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08978523
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TELEPHONE: To NO:
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Best Local Similarity 95.3%;
Matches 183; Conservative
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STATE: DC
COUNTRY: USA
20005
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SEQUENCE
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                                                                                                               1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                            Gaps
                   1;
 Length 193;
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
                   Indels
                                                                                                                                                                                                                                                           Sequence 3, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICAMT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
Score 1343; DB 1; I
Pred. No. 7.37e-111;
7; Mismatches 1;
                                                                                                                                                                                            193 AA.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNES/AGENT INFORMATION:
NAME: ESMONDA, ROBERT W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 193 AA; 20820 MW; 185063 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECOMMUNICATION INCORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              Sequence 3, Application US/08978523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 193 amino acids
                                                                                                                                                                                           STANDARD;
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Query Match 96.9%;
Best Local Similarity 95.3%;
Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                              CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                        181 GALVTVGAFFASK 193
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US-08-978-523-3
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                                            1; Gaps
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Score 1343; DB 2; Length 193;
Pred. No. 7.37e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
GENERAL GUASTELLANT:
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1337; DB 1; Length 193;
Pred. No. 2.65e-110;
8; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798 897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REEFENCE/DOCKET NUMBER: 1483.0140001
TELEPHONE: 202-371-2600
                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 AA.
                                          7; Mismatches
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ENCE 193 AA; 20832 MW; 183365 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08798897
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INFORMATION FOR SEQ ID NO: 4:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 193 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
Query Match 96.9%;
Best Local Similarity 95.3%;
Matches 184; Conservative
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Best Local Similarity 94.3%;
Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                 180 GALVTVGAFFASK 192
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Fri Jun 23 14:19:56 2000; MasPar time 5.42 Seconds 511.832 Million cell updates/sec MPsrch_pp Run on:

Tabular output not generated.

>US-09-155-327B-9 (1-192) from USO9155327B.pep 1386 1 MPTPASTPDTRALVADFVGY......VTGAVALGALVTVGAFFASK 192

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

145341 seqs, 14437480 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1 Database:

Mean 30.635; Variance 141.077; scale 0.217 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Pred. No.	nce 3, Applicatio 7.37e-111 nce 4, Applicatio 2.65e-110 nce 5, Applicatio 7.67e-110 nce 5, Applicatio 7.67e-110 nce 6, Applicatio 7.67e-110 nce 6, Applicatio 7.67e-110 nce 7, Applicatio 2.75e-109 nce 7, Applicatio 7.82e-45 nce 14, Applicati 7.82e-45 nce 14, Applicati 7.82e-45 nce 59, Applicati 7.82e-45 nce 23, Applicati 7.82e-45 nce 24, Applicati 7.82e-45 nce 23, Applicati 7.82e-45 nce 23, Applicati 7.82e-45 nce 23, Applicati 8.61e-39 nce 10, Applicati 8.61e-39 nce 10, Applicati 8.61e-39
Descr	15. 08 - 998 - Sequence US-08-998 - Sequence US-08-978 - Sequence US-08-470 - Sequence US-08-471 - Sequence US-08-61 - Sequence US-08-61 - Sequence US-08-61 - Sequence US-08-61 - Sequence US-08-607
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~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	ALIGNMEN US-08-798-897-3 STANDARD; P XXXXXX Sequence 3, Application US/08798897 SEGUENCES CONTITION Genes Codi TITLE OF INVENTION: Genes Codi TITLE OF INVENTION: Homologue NUMBER OF SEQUENCES: 53 CORRESPONDENCE SS: ADDRESSEE: STERNE, KESSLER, STREET: 1100 New York Avenue CITY: Washington STARTE: DC COUNTRY: USA ZIP: 20005 COUNTRY: USA ZIP: 20005 COMPUTER: THE PROPED GOOD TOOS/NS- SOFTWARE: PatentIn Release # COMPUTER: PatentIN Release # TING DATE: February 11, 19 CLASSIFICATION NUMBER: 148 REGISTATION NUMBER: 13, 893 REFERENCE/DOCKET NUMBER: 148 TELECOMMUNICATION INFORMATION: TELEPAN: 200-371-260 TELECANION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 193 amino acids TYPE: amino acid STRANDEDNESS: not relevant TOPPLOGGY: linear MOLECULE TYPE: protein
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